

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2001, 09:00:04 ; Search time 41.13 seconds
(without alignments)
208.911 Million cell updates/sec

Title: US-09-889-300A-1
Perfect score: 614
Sequence: 1 QVQLQSGAELVRPGTSVKV.....ARDGPWFAYWGQGLTVTSA 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101.*
1: /SID52/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID52/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID52/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID52/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID52/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID52/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID52/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID52/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID52/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID52/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID52/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID52/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID52/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID52/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID52/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID52/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID52/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID52/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID52/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID52/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID52/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	614	100.0	116	21	Murine monoclonal
2	554.5	90.3	119	19	Amino acid sequenc
3	554.5	90.3	138	14	Mouse C4G1 Ig heav
4	554.5	90.3	138	19	Variable region of
5	546.5	89.0	119	18	Lead binding MAb 1
6	515	83.9	137	12	Heavy chain variab
7	515	83.9	137	12	Mouse MAb 4D12 H c
8	515	83.9	141	11	ME4 Heavy Chain V
9	515	83.9	141	18	MAb ME4 heavy chai
10	515	83.9	141	20	Mouse ME4 heavy cha
11	510.5	83.1	138	18	Variable heavy cha

12	503.5	82.0	119	19	AAW49813	Amino acid sequenc
13	503.5	82.0	121	18	AAW07437	Anti-DNA antibody
14	503.5	82.0	222	14	AAR39267	Humanised C4G1 Ig
15	503.5	82.0	222	19	AAW49817	Fragment of humani
16	503.5	82.0	235	14	AAR39268	Humanised C4G1 Ig
17	503.5	82.0	235	19	AAW49818	Amino acid sequenc
18	503.5	82.0	449	14	AAR43339	Completely humanis
19	503.5	82.0	449	19	AAW49816	Amino acid sequenc
20	498.5	81.2	136	8	AAW70624	Sequence encoded b
21	498.5	81.2	136	18	AAW10584	Anti-Hepatitis B h
22	498.5	81.2	136	18	AAW16340	Mouse-human chimae
23	498.5	81.2	136	18	AAW10239	Chimeric anti-hepa
24	498.5	81.2	136	19	AAW47510	Human anti-hepatit
25	498.5	81.2	136	19	AAW41054	Human anti-hepatit
26	498.5	81.2	136	19	AAW47517	Human anti-hepatit
27	498.5	81.2	136	20	AAW89535	Chimeric anti-hepa
28	498.5	81.2	136	22	AAB98085	Chimeric anti-hepa
29	497.5	81.0	117	17	AAR88716	Mouse antibody hea
30	492	80.1	272	17	AAW00557	Nematode salivary
31	492	80.1	272	19	AAW43913	Mus musculus antib
32	490.5	79.9	119	18	AAW01585	Lead binding MAB 1
33	490.5	79.9	121	17	AAW00833	Variable heavy cha
34	487.5	79.4	117	14	AAR35032	GMP-140 MAB heavy
35	487.5	79.4	123	21	AAW78325	Anti-zeta-chain an
36	487.5	79.4	532	21	AAW78328	Bispecific anti-ze
37	487	79.3	1050	21	AAB09774	Molecular pathogen
38	485	79.0	114	13	AAR21273	Murine VH group 1
39	484	78.8	114	13	AAR21277	Murine VH group 1
40	483	78.7	118	18	AAW27122	Murine antibody he
41	482.5	78.6	119	17	AAW04332	Heavy chain of mon
42	482.5	78.6	121	16	AAR74964	Anti-idiotypic anti
43	482	78.5	114	13	AAR21281	Murine VH group 1
44	481.5	78.4	119	21	AAW71473	Mouse monoclonal a
45	481	78.3	121	13	AAR28806	5A8 VH. Synthetic

ALIGNMENTS

RESULT 1
AAB10443
ID AAB10443 standard; protein; 116 AA.
XX
AC AAB10443;
XX
DT 01-DEC-2000 (first entry)
XX
DE Murine monoclonal antibody MAK HE2 variable region heavy chain.
XX
KW Murine; monoclonal antibody; MAK HE2; heavy chain; variable region;
KW human cellular membrane antigen; tumor associated antigen; TAA;
KW vaccine; cancer.
XX
OS Mus sp.
XX
PN WO200041722-A1.
XX
PD 20-JUL-2000.
XX
PF 12-JAN-2000; 2000WO-EP00174.
XX
PR 13-JAN-1999; 99CH-0000051.
XX
PA (IGEN-) IGENEON GMBH.
XX
PI Eckert H, Loibner H;
XX
DR WPI; 2000-475956/41.
XX
PT Novel use of antibodies against human cellular membrane antigens for
PT vaccination against cancer
XX
PS Example 3; Page 47; 54pp; German.

XX This invention describes the novel use of an antibody targeted to a
 CC human cellular membrane antigen, to manufacture a medicament to
 CC prophylactically and/or therapeutically vaccinate against cancer.
 CC The antibodies against tumor associated antigen (TAA) for prophylactic
 CC and/or therapeutic vaccination against cancer may be used in low doses
 CC (when compared to antibodies against TAA for passive immunotherapy),
 CC typically less than 1 mg by injection. The antibodies also have a life
 CC continual activity that directly induces immunity and their shelf life
 CC is unlimited (fresh vaccination is always possible). This sequence
 CC represents the murine monoclonal antibody MAK HE2 variable region heavy
 CC chain fragment which is used in the method of the invention.
 XX
 SQ Sequence 116 AA;

Query Match 100.0%; Score 614; DB 21; Length 116;
 Best Local Similarity 100.0%; Pred. No. 2.1e-47;
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGAEIVRPGTSVKYSCASGYAFNLYLIEWVKQRPQGLEWVINGVINGSGGTNY 60
 Db 1 qvqlqsgaeivrpqtsvkyscasgyafnlyliewvkqrpqgglewvngvngsggtny 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDGPWFAYWGQGLTIVTVA 116
 Db 61 nekfkgtatltdkssstaymqllssltssdsavycardgwpwfaywgqglitvtva 116

RESULT 2
 AAW49814
 ID AAW49814 standard; Protein; 119 AA.
 XX
 AC AAW49814;
 XX
 DT 24-SEP-1998 (first entry)
 XX
 DE Amino acid sequence of the mouse antibody C4G1 mature heavy chain.
 XX
 KW Heavy chain; humanised; immunoglobulin; Ig; mouse C4G1; antibody;
 KW inhibition; antigen; cardiovascular disease; thromboembolic disorder;
 KW cancer; acute myocardial infarction; unstable angina; stroke;
 KW transient ischemic episode; pulmonary embolism; deep vein thrombosis;
 KW extracorporeal cardiopulmonary circulation.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Domain 31..35
 FT Domain /note= "complementarity determining region"
 FT Domain 50..66
 FT Domain /note= "complementarity determining region"
 FT Domain 99..108
 FT Domain /note= "complementarity determining region"
 XX
 XX US5777085-A.
 XX
 XX 07-JUL-1998.
 XX
 XX 17-MAY-1995; 95US-0458516.
 XX
 XX 03-MAY-1993; 93US-0059159.
 XX 20-DEC-1991; 91US-0812111.
 XX 09-JUN-1992; 92US-0895952.
 XX 11-SEP-1992; 92US-0944159.
 XX
 XX (PROT-) PROTEIN DESIGN LABS INC.
 XX
 XX Co MS, Tso JY;
 XX
 XX WPI; 1998-398136/34.
 XX
 XX New humanised immunoglobulin which binds GPIIb/IIIa - derived from

PT mouse C4G1 antibody, used for inhibiting platelet aggregation for
 PT treating cardiovascular and thromboembolic disorders.
 XX
 PS Claim 1; Fig 5B; 35pp; English.
 XX
 CC This is the amino acid sequence of the humanised antibody C4G1 heavy
 CC chain, used in the method of the invention involving the creation
 CC of a humanised immunoglobulin (Ig) derived from the mouse C4G1 antibody.
 CC The humanised Ig is capable of binding to GPIIb/IIIa and inhibiting
 CC platelet aggregation and also the releasing reaction of platelets. The
 CC Ig can be used for treating cardiovascular diseases and thromboembolic
 CC disorders, e.g. acute myocardial infarction, unstable angina, stroke,
 CC transient ischemic episodes, deep vein thrombosis and pulmonary embolism,
 CC extracorporeal cardiopulmonary circulation. The Ig can also be used in
 CC diagnosing the presence and location of a thrombus, or certain types of
 CC cancer cells which develop GPIIb/IIIa on their surfaces, for the
 CC detection of GPIIb/IIIa antigen or for isolating platelets.
 XX
 SQ Sequence 119 AA;

Query Match 90.3%; Score 554.5; DB 19; Length 119;
 Best Local Similarity 91.6%; Pred. No. 4.1e-42;
 Matches 109; Conservative 3; Mismatches 4; Indels 3; Gaps 2;

QY 1 QVQLQSGAEIVRPGTSVKYSCASGYAFNLYLIEWVKQRPQGLEWVINGVINGSGGTNY 60
 Db 1 qvqlqsgaeivrpqtsvkyscasgyafnlyliewvkqrpqgglewvngvngsggtny 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCA-RDG--PWFAYWGQGLTIVTVA 116
 Db 61 nekfkgtatltdkssstaymqllssltssdsavycardgngwgfaywrgtltvtva 119

RESULT 3
 AAR39266
 ID AAR39266 standard; Protein; 138 AA.
 XX
 AC AAR39266;
 XX
 DT 29-NOV-1993 (first entry)
 XX
 DE Mouse C4G1 Ig heavy-chain.
 XX
 KW Immunoglobulin; H-chain; platelet membrane glycoprotein; GPIIb/IIIa;
 KW monoclonal antibody; platelet agglutination; humanised antibody.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein /label= signal_peptide
 FT Region 21..138
 FT Region /label= light_chain
 FT Region 50..54
 FT Region /label= complementarity_determining_region_1
 FT Region 69..85
 FT Region /label= CDR_2
 FT Region 118..127
 FT Region /label= CDR_3
 XX
 XX WO9313133-A.
 XX
 XX 08-JUL-1993.
 XX
 XX 15-DEC-1992; 92WO-JP01630.
 XX
 XX 20-DEC-1991; 91US-0812111.
 XX 09-JUN-1992; 92US-0895952.
 XX 11-SEP-1992; 92US-0944159.
 XX
 XX (PROT-) PROTEIN DESIGN LABS INC.
 XX
 XX (YAMA) YAMANOUCHI PHARM CO LTD.

```
XX Co MS, Tso JY;
PI WPI; 1993-227275/28.
XX N-PSDB; AAQ45663.
XX Compsn. contg. immunoglobulin specific for the GP-IIIB and -IIIA
PT protein - for treating disorders related to vascular thrombosis
XX Disclosure; Fig 2B; 54pp; Japanese.
XX This is the sequence of the mouse C4G1 immunoglobulin heavy
CC chain. See AAR39265 for the light chain sequence. The antibody is
CC specific for the GPIIb/IIIa protein and inhibits platelet
CC agglutination. The Ig is thus useful in the treatment of
CC thrombosis.
XX Sequence 138 AA;
SQ
Query Match 90.3%; Score 554.5; DB 14; Length 138;
Best Local Similarity 91.6%; Pred. No. 4.8e-42;
Matches 109; Conservative 3; Mismatches 4; Indels 3; Gaps 2;
QY 1 QVQLQQSGAELVRPGTSVKVSKCKASGYAFTNYLIEWVKRPGQGLEWIGVINPQSGGTNY 60
Db 20 QVQLQSGAELVPGTSVRSVSKCKASGYAFTNYLIEWVKRPGQGLEWIGVINPQSGGTNY 79
QY 61 NEKFYKATLTADKSSSTAYMOLSLTSDSAVYFCA-RDG--PWFAYWGQGLTLVTSA 116
Db 80 NEKFYKATLTVDKSTTAYMQLSLTSDSAVYFCARRDGNYGWFAYWGRGLTLVTSA 138
RESULT 4
AAW49810
ID AAW49810 standard; Protein; 138 AA.
XX
AC AAW49810;
DT 24-SEP-1998 (first entry)
XX
DE Variable region of mouse antibody C4G1 light chain.
XX
KW Mouse; antibody C4G1; heavy chain; humanised; immunoglobulin; Ig;
KW inhibition; antigen; cardiovascular disease; thromboembolic disorder;
KW cancer; acute myocardial infarction; unstable angina; stroke;
KW transient ischemic episode; pulmonary embolism; deep vein thrombosis;
KW extracorporeal cardiopulmonary circulation.
XX
OS Mus sp.
XX
PH Key Location/Qualifiers
FT Peptide 1..19
FT Protein 20..138
FT /note= "mature protein"
FT Domain 50..54
FT /note= "complementarity determining region"
FT Domain 69..85
FT /note= "complementarity determining region"
FT Domain 118..127
FT /note= "complementarity determining region"
XX
PN US5777085-A.
XX
PD 07-JUL-1998.
XX
PF 17-MAY-1995; 95US-0458516.
XX
PR 03-MAY-1993; 93US-0059159.
PR 20-DEC-1991; 91US-0812111.
PR 09-JUN-1992; 92US-0895952.
PR 11-SEP-1992; 92US-0944159.
XX
```

```
PA (PROT-) PROTEIN DESIGN LABS INC.
XX Co MS, Tso JY;
PI WPI; 1998-398136/34.
XX N-PSDB; AAV36742.
XX New humanised immunoglobulin which binds GPIIb/IIIa - derived from
PT mouse C4G1 antibody, used for inhibiting platelet aggregation for
PT treating cardiovascular and thromboembolic disorders.
XX Disclosure; Fig 2B; 35pp; English.
XX This is the amino acid sequence of the mouse antibody C4G1 heavy
CC chain, used in the method of the invention involving the creation
CC of a humanised immunoglobulin (Ig) derived from the mouse C4G1 antibody.
CC The humanised Ig is capable of binding to GPIIb/IIIa and inhibiting
CC platelet aggregation and also the releasing reaction of platelets. The
CC Ig can be used for treating cardiovascular diseases and thromboembolic
CC disorders, e.g. acute myocardial infarction, unstable angina, stroke,
CC transient ischemic episodes, deep vein thrombosis and pulmonary embolism,
CC extracorporeal cardiopulmonary circulation. The Ig can also be used in
CC diagnosing the presence and location of a thrombus, or certain types of
CC cancer cells which develop GPIIb/IIIa on their surfaces, for the
CC detection of GPIIb/IIIa antigens or for isolating platelets.
XX Sequence 138 AA;
SQ
Query Match 90.3%; Score 554.5; DB 19; Length 138;
Best Local Similarity 91.6%; Pred. No. 4.8e-42;
Matches 109; Conservative 3; Mismatches 4; Indels 3; Gaps 2;
QY 1 QVQLQQSGAELVRPGTSVKVSKCKASGYAFTNYLIEWVKRPGQGLEWIGVINPQSGGTNY 60
Db 20 QVQLQSGAELVPGTSVRSVSKCKASGYAFTNYLIEWVKRPGQGLEWIGVINPQSGGTNY 79
QY 61 NEKFYKATLTADKSSSTAYMOLSLTSDSAVYFCA-RDG--PWFAYWGQGLTLVTSA 116
Db 80 NEKFYKATLTVDKSTTAYMQLSLTSDSAVYFCARRDGNYGWFAYWGRGLTLVTSA 138
RESULT 5
AAW01580
ID AAW01580 standard; Protein; 119 AA.
XX
AC AAW01580;
DT 22-AUG-1997 (first entry)
XX
DE Lead binding MAb 14F11 heavy chain variable region.
XX
KW Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
KW pharmaceutical; health care; skin treatment; pesticide; herbicide;
KW heavy metal.
XX
OS Mus musculus.
XX
PN W09639518-A1.
XX
PD 12-DEC-1996.
XX
PF 05-JUN-1996; 96WO-US09258.
XX
PR 10-OCT-1995; 95US-0541373.
PR 05-JUN-1995; 95US-0462798.
XX
PA (BION-) BIONEERASKA INC.
XX
PI Lopez O, Murray PJ, Wylie DE;
XX WPI; 1997-043140/04.
DR N-PSDB; AAT58254.
```



```
Oy 1 QVQLQQSGAEILVRPCTSVKVSCKASGYAFTNVLIEWVKRPGQGLEWIGVINPGSGGTNY 60
  || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 qvhlqsggaemvrpqtsvkvsctsgyafntyliewvkqrpqgglewlgvinpssggtty 79
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Oy 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSASVYFCARDGPWFA--YWGQGTFLVTVA 116
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 nekfkdkttadkssstaysmhlsltsdssavylcartsgshalelywgqgtsvtvss 137
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
AAR09427
ID AAR09427 standard; Protein; 141 AA.
XX
AC AAR09427;
XX
DT 04-MAR-1993 (first entry)
XX
DE ME4 Heavy Chain V Region (mouse).
XX
KW Monoclonal antibody; chimera; light; heavy; chain; constant;
KW variable; antigen; diagnosis; cancer; tumour.
XX
OS Mus musculus.
XX
PN WO9002569-A.
XX
PD 22-MAR-1990.
XX
PF 06-SEP-1989; 89WO-US03852.
XX
PR 06-SEP-1988; 88US-0240624.
PR 08-SEP-1988; 88US-0241744.
PR 13-SEP-1988; 88US-0243739.
PR 04-OCT-1988; 88US-0253002.
PR 19-JUN-1989; 89US-0367641.
PR 21-JUL-1989; 89US-0382768.
XX
PA (ITGE-) INT GENETIC ENG INC.
XX
PI Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
XX
DR WPI; 1990-115825/15.
DR N-PSDB; AAQ08609.
XX
PT Chimeric mouse-human antibodies - prepd. using genes coding for
PT constant human region murine variable region, esp. to 3 tumour
PT antigen
XX
PS Claim 13; Page 123 + Fig 30; 173pp; English.
XX
CC The sequence is used in the prodn. of a chimeric antibody mol.
CC comprising two light chains and two heavy chains, each having a
CC constant region (human) and a variable region (murine) having
CC specificity to an antigen bound by murine monoclonal antibody
CC (Mab) B38.1. The chimeric antibodies can be used for any purpose for
CC which the original murine MAb can be used, with the advantage that
CC they are more compatible with the human body. They are esp. used for
CC the diagnosis and treatment of cancer.
XX
SQ Sequence 141 AA;

Query Match 83.9%; Score 515; DB 11; Length 141;
Best Local Similarity 85.0%; Pred. No. 1.6e-38;
Matches 102; Conservative 4; Mismatches 10; Indels 4; Gaps 2;

Oy 1 QVQLQQSGAEILVRPCTSVKVSCKASGYAFTNVLIEWVKRPGQGLEWIGVINPGSGGTNY 60
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 qvhlqsggaemvrpqtsvkvsctsgyafntyliewvkqrpqgglewlgvinpssggtty 79
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Oy 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSASVYFCARD--GPWFA--YWGQGTFLVTVA 116
  || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
Db 80 nenfkgtatltdkssstsymqlsltsdssavylfcarghygggyfvmddywgqgtsvtvsa 139
  || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT 9
AAW06216
ID AAW06216 standard; Protein; 141 AA.
XX
AC AAW06216;
XX
DT 13-FEB-1997 (first entry)
XX
DE MAb ME4 heavy chain variable region.
XX
KW Chimeric antigen; monoclonal antibody; ME4: antibody engineering;
KW tumour; antigen; breast carcinoma; colon carcinoma; lung carcinoma;
KW ovary carcinoma; melanoma; cancer; diagnosis; therapy; heavy chain.
XX
OS Mus sp.
XX
PN US5576184-A.
XX
PD 19-NOV-1996.
XX
PF 06-SEP-1988; 88US-0240624.
XX
PR 06-MAY-1991; 91US-0659401.
PR 06-SEP-1988; 88US-0240624.
PR 08-SEP-1988; 88US-0241744.
PR 13-SEP-1988; 88US-0243739.
PR 04-OCT-1988; 88US-0253002.
PR 19-JUN-1989; 89US-0367641.
PR 21-JUL-1989; 89US-0382768.
PR 27-DEC-1994; 94US-0364001.
XX
PA (XOMA ) XOMA CORP.
XX
PI Better MD, Chang CP, Horwitz AH, Lei S, Robinson RR;
XX
DR WPI; 1997-011249/01.
DR N-PSDB; AAT43441.
XX
PT Chimeric mouse-human antibodies - recognise a human tumour antigen,
PT used for the treatment and diagnosis of human cancers
XX
PS Example 3; Fig 30; 102pp; English.
XX
CC The heavy chain variable region (AAW06216) of mouse monoclonal
CC antibody ME4 is the product of a cDNA clone (AAT43441) isolated
CC from a ME4 hybridoma cDNA library. Mab ME4 (IgG1) binds to an
CC antigen that is expressed on the surface of human lung, breast,
CC colon and ovary carcinomas and melanomas, but not on most normal
CC adult tissues. The heavy chain and light chain variable regions
CC (see also AAW06215) of ME4 can be linked to human constant regions
CC and expressed in transformed host cells. Novel mouse-human
CC chimeric antibodies (see also AAW06209-14 and AAW06217-18) can be
CC produced that have specificity to human tumour antigens for use in
CC the treatment and diagnosis of human cancer.
XX
SQ Sequence 141 AA;

Query Match 83.9%; Score 515; DB 18; Length 141;
Best Local Similarity 85.0%; Pred. No. 1.6e-38;
Matches 102; Conservative 4; Mismatches 10; Indels 4; Gaps 2;

Oy 1 QVQLQQSGAEILVRPCTSVKVSCKASGYAFTNVLIEWVKRPGQGLEWIGVINPGSGGTNY 60
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 qvhlqsggaemvrpqtsvkvsctsgyafntyliewvkqrpqgglewlgvinpssggtty 79
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Oy 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSASVYFCARD--GPWFA--YWGQGTFLVTVA 116
  || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 nenfkgtatltdkssstsymqlsltsdssavylfcarghygggyfvmddywgqgtsvtvsa 139
  || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

RESULT 10

AAW85063
ID AAW85063 standard; Protein; 141 AA.

XX AC AAW85063;

XX 16-APR-1999 (first entry)

XX Mouse ME4 heavy chain variable region.

XX Heavy chain variable region; murine antibody ME4; antibody ING-1;
KW chimeric immunoglobulin; human tumour antigen; chimeric antibody;
KW treatment; human cancer.

XX OS Mus sp.

XX PN US5843685-A.

XX PD 01-DEC-1998.

XX PF 06-JUN-1995; 95US-0466034.

XX PR 06-SEP-1989; 89WO-US03852.

XX PR 06-SEP-1988; 88US-0240624.

XX PR 08-SEP-1988; 88US-0241744.

XX PR 13-SEP-1988; 88US-0243739.

XX PR 04-OCT-1988; 88US-0253002.

XX PR 19-JUN-1989; 89US-0367641.

XX PR 21-JUL-1989; 89US-0382768.

XX PR 27-DEC-1994; 94US-0364001.

XX PR 06-JUN-1995; 95US-0466034.

XX PA (XOMA) XOMA CORP.

XX PI Better MD, Chang CP, Horwitz AH, Lei S, Robinson RR;

XX WPI; 1999-044574/04.

XX DR N-PSDB; AAV71159.

XX PT Chimeric antibody specific for human tumour antigen - useful as

PT immunoassay, imaging or antitumour agent

XX PS Example 3; Fig 30; 92pp; English.

XX CC The present sequence represents the heavy chain variable region of

CC murine antibody ME4. The sequence was used to create chimeric

CC mouse-human immunoglobulins which recognise the human tumour

CC antigen bound by antibody ING-1 (produced by hybridoma cell line

CC ATCC HB 9812). The chimeric antibodies also have an antigen-binding

CC site that competitively inhibits the binding of antibody ING-1, and

CC mediate complement-dependent cytotoxicity of target cells or

CC antibody-dependent cellular cytotoxicity to target cells. The

CC chimeric antibodies can be used for therapeutic purposes in the

XX treatment of human cancer.

RESULT 11

AAW34515

ID AAW34515 standard; Protein; 138 AA.

XX AC AAW34515;

XX DT 19-MAR-1998 (first entry)

XX Variable heavy chain of antibody from hybridoma 5-465-210.

XX Variable region coding sequence; constant region epitope; hybridoma;
KW antibody detection; antigen/antibody complex; variable heavy chain.

XX OS Mus musculus.

XX PN W09727486-A1.

XX PD 31-JUL-1997.

XX PF 17-JAN-1997; 97WO-US01074.

XX PR 23-JAN-1996; 96US-0589939.

XX PA (ABBO) ABBOTT LAB.

XX Golden AM, Hackett JR, Hoff JA, Ostrow DH;

XX WPI; 1997-393833/36.

XX DR N-PSDB; AAT98832.

XX PT Use of antibody constant region epitope(s) - as control or

PT calibrator reagents in assays for detecting the presence of an

XX antibody in a test sample

XX PS Disclosure; Page 60; 109pp; English.

XX CC This sequence represents the variable heavy chain of the antibody
CC produced by hybridoma 5-465-210, and can be detected using the method of
CC the invention. The method is for detecting the presence of antibody which
CC may be present in a test sample. It comprises contacting a test sample
CC suspected of containing the antibody with an antigen specific for the
CC antibody to allow the formation of antigen/antibody complexes, detecting
CC the presence of the antibody which may be present in the test sample and
CC employing, as a control or calibrator, a reagent which binds to the
CC antigen. The improvement to this method over previous methods, comprises
CC employing, as the control or calibrator, a reagent comprising one or more
CC antibody constant region epitopes, where the reagent binds to the antigen
CC and is homogeneous with respect to specificity and affinity. The method
CC can be also be used for detecting the presence of antibodies developed
CC against more than one antigen. The method is used particularly for the
CC detection of human antibodies specific for a given antigen, e.g. HIV-1,
CC hepatitis E virus, rubella virus, etc. Use of the reagents circumvent all
CC of the problems associated with using an immune sera in the manufacture
CC of calibrators and positive controls. The present reagents can be readily
CC and reproducibly generated in virtually unlimited quantities and are also
CC useful for quantitating, and monitoring the integrity of, the antigen
CC used in assays.

XX SQ Sequence 138 AA;

Query Match 83.9%; Score 515; DB 20; Length 141;
Best Local Similarity 85.0%; Pred. No. 1.6e-38;
Matches 102; Conservative 4; Mismatches 10; Indels 4; Gaps 2;

QY 1 OVQLQSGAELVRPGTSVKVSKKASGYAFNTNLIIEWKORPGGLEWIGVINGSGGTNY 60

Db 20 qvhlqsgaelvrpgtsvkvscktsyafntnlmewkprpggglewivngpsgdaky 79

QY 61 NEFKGKATLTADKSSSTAYMQLSSLTSDSVAIFYFCAR--GPWFA--YWGQTLVTVSA 116

Db 80 nenfkgkatltadksstaysmqlssltssdsavfycarghyggfymdywgqgtsvtvsa 139

Query Match 83.1%; Score 510.5; DB 18; Length 138;
Best Local Similarity 84.9%; Pred. No. 3.8e-38;
Matches 101; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

QY 1 OVQLQSGAELVRPGTSVKVSKKASGYAFNTNLIIEWKORPGGLEWIGVINGSGGTNY 60

Db 20 qvhlqsgaelvrpgtsvkvscktsyafntnlmewkprpggglewivngpsgfty 79

QY 61 NEFKGKATLTADKSSSTAYMQLSSLTSDSVAIFYFCAR--DGPWFAYWGQTLVTVSA 116

Db 80 nekfgkatltadksstaysmqlssltssdsavfycartivtdydywgqgtpvtvss 138

SQ Sequence 121 AA;

Query Match 82.0%; Score 503.5; DB 18; Length 121;
 Best Local Similarity 82.5%; Pred. No. 1.4e-37;
 Matches 99; Conservative 3; Mismatches 13; Indels 5; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKKASGYAFNTYLIIEWKQRPQGGLIEWIGVINPGSGGTNY 60
 ||||| ||||| :||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 qvqlqsgaelvrpgtsvkvsckasgyafntyliewkrpqqggliewigviyppsggtnty 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDG-----PWFAYWGQGLTLTVTS 115
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 qvqlqsgaelarpgasvklscasgytftsygswkrtgggliewigviyppsggtntyy 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDG-----PWFAYWGQGLTLTVTS 115
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 61 nekfkgtatltdkssstaymqllssltssdsavycfargsyyswfwaygggtlvtvs 120

RESULT 14
 AAR39267
 ID AAR39267 standard; Protein; 222 AA.
 XX
 AC AAR39267;
 XX
 DT 29-NOV-1993 (first entry)
 XX
 DE Humanised C4G1 Ig heavy-chain Fab fragment.
 XX
 KW Immunoglobulin; H-chain; platelet membrane glycoprotein; GPIIa/IIIB;
 KW monoclonal antibody; platelet agglutination; humanised antibody.
 KW
 XX Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT Region 31..35
 FT
 FT /label= complementarity_determining_region_1
 FT Region 50..66
 FT /label= CDR_2
 FT Region 99..108
 FT /label= CDR_3
 FT
 XX W09313133-A.
 XX
 XX 08-JUL-1993.
 XX
 XX 15-DEC-1992; 92WO-JP01630.
 XX
 XX 20-DEC-1991; 91US-0812111.
 PR 09-JUN-1992; 92US-0895952.
 PR 11-SEP-1992; 92US-0944159.
 XX
 XX (PROT-) PROTEIN DESIGN LABS INC.
 PA (YAMA) YAMANOUCHI PHARM CO LTD.
 XX
 XX Co MS, Tso JY;
 XX
 XX WPI; 1993-227275/28.
 XX
 XX Composn. contg. immunoglobulin specific for the GP-IIIB and -IIIA
 PT protein - for treating disorders related to vascular thrombosis
 XX
 XX Disclosure; Fig 7C; 54pp; Japanese.
 PS
 PS This is the sequence of the humanised C4G1 immunoglobulin heavy
 CC chain Fab fragment. See AAR39268 for the F(ab')2 sequence. The
 CC antibody is specific for the platelet membrane glycoprotein
 CC GPIIa/IIIB and inhibits platelet agglutination. The Ig is thus
 CC useful in the treatment of thrombosis.
 CC
 XX
 XX Sequence 222 AA;

Query Match 82.0%; Score 503.5; DB 14; Length 222;
 Best Local Similarity 80.7%; Pred. No. 2.6e-37;
 Matches 96; Conservative 12; Mismatches 8; Indels 3; Gaps 2;

QY 1 QVQLQSGAELVRPGTSVKVSKKASGYAFNTYLIIEWKQRPQGGLIEWIGVINPGSGGTNY 60
 ||||| ||||| :||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 qvqlqsgaelvrpgtsvkvsckasgyafntyliewkrpqqggliewigviyppsggtnty 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCA-RDG--PWFAYWGQGLTLTVTSA 116
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 61 nekfgkgrvltvdestntaymelsslrtsedavycfarrdngywfaywggtlvtvss 119

RESULT 15
 AAW49817
 ID AAW49817 standard; Protein; 222 AA.
 XX
 AC AAW49817;
 XX
 DT 24-SEP-1998 (first entry)
 XX
 DE Fragment of humanised antibody C4G1 heavy chain.
 XX
 KW Humanised antibody C4G1; heavy chain; humanised; immunoglobulin; Ig;
 KW mouse C4G1; antibody; inhibition; antigen; cardiovascular disease;
 KW thromboembolic disorder; cancer; acute myocardial infarction;
 KW unstable angina; stroke; transient ischemic episode; pulmonary embolism;
 KW deep vein thrombosis; extracorporeal cardiopulmonary circulation.
 XX
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX
 PN US5777085-A.
 XX
 PD 07-JUL-1998.
 XX
 PF 17-MAY-1995; 95US-0458516.
 XX
 PR 03-MAY-1993; 93US-0059159.
 PR 20-DEC-1991; 91US-0812111.
 PR 09-JUN-1992; 92US-0895952.
 PR 11-SEP-1992; 92US-0944159.
 XX
 XX (PROT-) PROTEIN DESIGN LABS INC.
 XX
 XX Co MS, Tso JY;
 XX
 XX WPI; 1998-398136/34.
 XX
 XX New humanised immunoglobulin which binds GPIIb/IIIa - derived from
 PT mouse C4G1 antibody, used for inhibiting platelet aggregation for
 PT treating cardiovascular and thromboembolic disorders.
 XX
 XX Disclosure; Fig 7C; 35pp; English.
 XX
 XX This is the amino acid sequence of a fragment of humanised antibody
 CC C4G1 heavy chain, used in the method of the invention involving the
 CC creation of a humanised immunoglobulin (Ig) derived from the mouse
 CC C4G1 antibody. The humanised Ig is capable of binding to GPIIb/IIIa
 CC and inhibiting platelet aggregation and also the releasing reaction of
 CC platelets. The Ig can be used for treating cardiovascular diseases and
 CC thromboembolic disorders, e.g. acute myocardial infarction, unstable
 CC angina, stroke, transient ischemic episodes, deep vein thrombosis and
 CC pulmonary embolism, extracorporeal cardiopulmonary circulation. The
 CC Ig can also be used in diagnosing the presence and location of a
 CC thrombus, or certain types of cancer cells which develop GPIIb/IIIa on
 CC their surfaces, for the detection of GPIIb/IIIa antigens or for
 CC isolating platelets.
 XX
 XX Sequence 222 AA;

Query Match 82.0%; Score 503.5; DB 19; Length 222;
 Best Local Similarity 80.7%; Pred. No. 2.6e-37;
 Matches 96; Conservative 12; Mismatches 8; Indels 3; Gaps 2;

Qy 1 QVLOQSGAELVRPCTSVKVSCKASGYAFTNYLIEWVKQRPQGGLIEWIGVINPGSGGTNY 60
Db 1 qvqvsgaevkpgssvksckasgyaftnyllwvvrqapqglwlgviypgsggtny 60
Qy 61 NEKFKGKATLTADKSSSTAYWQLSSLTSDSDSAVYFCA-RDG--PWFAWGGGTLVTVSA 116
Db 61 nekfggrvtltvdestntaymelsslrse dtavyfcarrdgnygw faywgg tlv tvss 119

Search completed: December 27, 2001, 09:01:00
Job time: 56 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2001, 09:00:04 ; Search time 22.67 seconds
(without alignments)
115.147 Million cell updates/sec

Title: US-09-889-300A-1
Perfect score: 614
Sequence: 1 QVQLQSGAELVRPGTSVKV.....ARDGPWFAYWGQGLTVTSA 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA: *
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pap: *
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pap: *
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pap: *
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pap: *
5: /cgn2_6/ptodata/2/iaa/PC1US_COMB.pap: *
6: /cgn2_6/ptodata/2/iaa/backfiles1.pap: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	554.5	90.3	119	1	US-08-458-516-11
2	554.5	90.3	138	1	US-08-458-516-7
3	546.5	89.0	119	3	US-08-767-128-10
4	510.5	83.1	138	3	US-08-589-939-1
5	503.5	82.0	119	1	US-08-458-516-10
6	503.5	82.0	222	1	US-08-458-516-22
7	503.5	82.0	235	1	US-08-458-516-23
8	503.5	82.0	449	1	US-08-458-516-13
9	497.5	81.0	117	4	US-09-157-370-2
10	490.5	79.9	119	3	US-08-767-128-20
11	485.5	79.1	121	3	US-08-881-037-65
12	485.5	78.6	119	2	US-08-737-560A-10
13	482	78.5	122	2	US-07-916-098A-10
14	480	78.2	137	1	US-08-392-419-2
15	478.5	77.9	123	1	US-08-497-312-15
16	478.5	77.9	123	2	US-08-560-558E-28
17	478	77.9	120	3	US-08-397-411-11
18	478	77.9	122	1	US-08-236-520-9
19	478	77.9	122	5	PCT-US95-05262-9
20	478	77.9	139	2	US-08-656-586-4
21	477	77.7	116	1	US-07-634-278-3
22	477	77.7	116	1	US-07-634-278-14
23	477	77.7	116	1	US-08-477-728-3
24	477	77.7	116	1	US-08-477-728-14
25	477	77.7	116	1	US-08-474-040-3
26	477	77.7	116	1	US-08-474-040-14
27	477	77.7	116	1	US-08-487-200-3

28	477	77.7	116	1	US-08-487-200-14	Sequence 14, Appl
29	477	77.7	116	1	US-08-488-113B-167	Sequence 167, App
30	477	77.7	116	1	US-08-477-484B-167	Sequence 167, App
31	477	77.7	116	1	US-08-107-669D-53	Sequence 53, Appl
32	477	77.7	116	1	US-08-472-788A-85	Sequence 85, Appl
33	477	77.7	116	2	US-08-477-531B-53	Sequence 53, Appl
34	477	77.7	116	2	US-08-646-360-167	Sequence 167, App
35	477	77.7	116	2	US-08-082-842A-85	Sequence 85, Appl
36	477	77.7	116	4	US-08-839-765-167	Sequence 167, App
37	477	77.7	116	4	US-09-136-389-167	Sequence 167, App
38	477	77.7	116	4	US-08-484-537-3	Sequence 3, Appli
39	477	77.7	116	4	US-08-484-537-14	Sequence 14, Appl
40	477	77.7	118	2	US-08-428-257A-74	Sequence 74, Appl
41	477	77.7	118	4	US-07-987-264-14	Sequence 14, Appl
42	477	77.7	239	3	US-08-279-772A-8	Sequence 8, Appli
43	477	77.7	239	4	US-08-902-486-11	Sequence 11, Appl
44	477	77.7	599	1	US-08-463-163-3	Sequence 3, Appli
45	476	77.5	122	3	US-08-767-128-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-458-516-11
; Sequence 11, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal fragment
; US-08-458-516-11

Query Match 90.3%; Score 554.5; DB 1; Length 119;
Best Local Similarity 91.6%; Pred. No. 3.3e-45;
Matches 109; Conservative 3; Mismatches 4; Indels 3; Gaps 2;

REFERENCE/DOCKET NUMBER: 11823-37-3
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-516-22

Query Match 82.0%; Score 503.5; DB 1; Length 222;
Best Local Similarity 80.7%; Pred. No. 3.9e-40;
Matches 96; Conservative 12; Mismatches 8; Indels 3; Gaps 2;
QY 1 QVQLQSGAELVRPGTSVKVSKKASGYAFTNLYLIEWVKORPGGLEWIGVINPGSGGTNY 60
Db 1 QVQLVQSGAEVKPGSSVKVSKKASGYAFTNLYLIEWVRQAPGGGLEWIGVIYVPGSGGTNY 60
QY 61 NEKFQKATLTADKSSSTAYMQLSLTSDSAVYFCA-RDG--PWFAYWGQGLTVTVA 116
Db 61 NEKFQKATLTADKSSSTAYMQLSLTSDSAVYFCA-RDG--PWFAYWGQGLTVTVA 119

RESULT 7
US-08-458-516-23
Sequence 23, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
APPLICANT: Tso, J. Yun
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-516-23

Query Match 82.0%; Score 503.5; DB 1; Length 235;
Best Local Similarity 80.7%; Pred. No. 4.1e-40;
Matches 96; Conservative 12; Mismatches 8; Indels 3; Gaps 2;
QY 1 QVQLQSGAELVRPGTSVKVSKKASGYAFTNLYLIEWVKORPGGLEWIGVINPGSGGTNY 60
Db 1 QVQLVQSGAEVKPGSSVKVSKKASGYAFTNLYLIEWVRQAPGGGLEWIGVIYVPGSGGTNY 60
QY 61 NEKFQKATLTADKSSSTAYMQLSLTSDSAVYFCA-RDG--PWFAYWGQGLTVTVA 116
Db 61 NEKFQKATLTADKSSSTAYMQLSLTSDSAVYFCA-RDG--PWFAYWGQGLTVTVA 119

RESULT 8
US-08-458-516-13
Sequence 13, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
APPLICANT: Tso, J. Yun
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-516-13

Query Match 82.0%; Score 503.5; DB 1; Length 449;
Best Local Similarity 80.7%; Pred. No. 8.4e-40;
Matches 96; Conservative 12; Mismatches 8; Indels 3; Gaps 2;
QY 1 QVQLQSGAELVRPGTSVKVSKKASGYAFTNLYLIEWVKORPGGLEWIGVINPGSGGTNY 60
Db 1 QVQLVQSGAEVKPGSSVKVSKKASGYAFTNLYLIEWVRQAPGGGLEWIGVIYVPGSGGTNY 60
QY 61 NEKFQKATLTADKSSSTAYMQLSLTSDSAVYFCA-RDG--PWFAYWGQGLTVTVA 116
Db 61 NEKFQKATLTADKSSSTAYMQLSLTSDSAVYFCA-RDG--PWFAYWGQGLTVTVA 119

RESULT 9

```
US-09-157-370-2
; Sequence 2, Application US/09157370A
; Patent No. 6262238
; GENERAL INFORMATION:
; APPLICANT: STEINBACHER, Stefan
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
; FILE REFERENCE: P8341-8072
; CURRENT APPLICATION NUMBER: US/09/157.370A
; EARLIER FILING DATE: 1998-09-21
; EARLIER FILING DATE: 1997-01-14
; EARLIER APPLICATION NUMBER: PCT/EP95/02626
; EARLIER FILING DATE: 1995-07-06
; EARLIER APPLICATION NUMBER: DE/P44 25 115.7
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-157-370-2

Query Match      81.0%; Score 497.5; DB 4; Length 117;
Best Local Similarity 80.3%; Pred. No. 7.1e-40;
Matches 94; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

Qy 1 OVQLOQSGAELVRPCTSVKVSCKASGYAFTNLYLIEWVKORPGQGLEWIGVINPGSGGTNY 60
   :||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EVQLOQSGGELVKPCASVKLSCKASGYFTSYMHMVKORPCGKLEWIGRINPGSGGTNY 60
   :||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 61 NEKFKGKATLTADKSSSTAYMOLSLTSDDSAVYFCARDG-PWFAYWGQGLTLVTVSA 116
   :||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 NEKFKGKATLTADKSSSTAYMOLSLTSDDSAVYFCARDG-PWFAYWGQGLTLVTVSS 117
   :||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
US-08-767-128-20
; Sequence 20, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767.128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996

US-09-157-370-2
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-767-128-20

Query Match      79.9%; Score 490.5; DB 3; Length 119;
Best Local Similarity 78.2%; Pred. No. 3.3e-39;
Matches 93; Conservative 10; Mismatches 13; Indels 3; Gaps 1;

Qy 1 OVQLOQSGAELVRPCTSVKVSCKASGYAFTNLYLIEWVKORPGQGLEWIGVINPGSGGTNY 60
   :||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 OVQLOQSGVELMKPCASVKISCKATGYTFSSYIEWVKORPGHGLEWIGELLPGSGGTNY 60
   :||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 61 NEKFKGKATLTADKSSSTAYMOLSLTSDDSAVYFCAR---DGPWFAYWGQGLTLVTVSA 116
   :||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 NEKFKGKATFTADTSNTAYMQVSLTSDSDSAVYVCARIYYGHLEWLFAYWGQGLTLVTSA 119
   :||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
US-08-881-037-65
; Sequence 65, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
; APPLICANT: Click, Gary D.
; APPLICANT: Swanson, Patrick C.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881.037
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Konski, Antoinette F.
; REGISTRATION NUMBER: 34,202
```

```
; REFERENCE/DOCKET NUMBER: 203442110710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-881-037-65

Query Match 79.1%; Score 485.5; DB 3; Length 121;
Best Local Similarity 80.0%; Pred. No. 9.7e-39;
Matches 96; Conservative 4; Mismatches 15; Indels 5; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFNLYLIEWYKQRPQGQGLEWIGVINFGSGGTNY 60
   ||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 QVQLLESGAELARPGASVKLSKASGYFTSYGISWVKQRTGQGLEWIGEILYPRSGNTYY 60

QY 61 NEKPKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDG-----PWFAYWGQGLTVTVS 115
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 NEKPKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARQSYYSYFWAYWGQGLTVTVS 120

RESULT 12
US-08-737-560A-10
; Sequence 10, Application US/08737560A
; Patent No. 5928893
; GENERAL INFORMATION:
; APPLICANT: KANG, Chang-Yuul
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KANG, Chang-Yuul
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
; STREET: Kwanaak-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 151-057
; ADDRESSEE: KIM, Joong-Gon
; STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 135-110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,560A
; FILING DATE: 13-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: KR 95-8176
; FILING DATE: 08-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-916-098A-10

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; OTHER INFORMATION: 4B4-1-1 heavy chain variable region
; US-08-737-560A-10

Query Match 78.6%; Score 482.5; DB 2; Length 119;
Best Local Similarity 79.0%; Pred. No. 1.8e-38;
Matches 94; Conservative 8; Mismatches 14; Indels 3; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFNLYLIEWYKQRPQGQGLEWIGVINFGSGGTNY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 QVQLQPGAELVRPGASVKLSKASGYTFSSYWMHWKQRPQGVLEWIGEINFGNGHTNY 60

QY 61 NEKPKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARD---GPWFAYWGQGLTVTVSA 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 NEKPKGKATLTVDKSSSTAYMQLSSLTSDSAVYYCARSETTARGFAYWGQGLTVTVSA 119

RESULT 13
US-07-916-098A-10
; Sequence 10, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET D.
; APPLICANT: ROSA, JOSEPH J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/916,098A
; FILING DATE: July 24, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08843
; FILING DATE: No. 5871732ember 27, 1991
; CLASSIFICATION: 424
; APPLICATION NUMBER: 07/618,542
; FILING DATE: No. 5871732ember 27, 1990
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN J. MC DONNELL
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,310-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; TELEX: 910/221-5317
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-916-098A-10
```



```
Query Match      78.5%; Score 482; DB 2; Length 122;
Best Local Similarity 72.1%; Pred. No. 2.le-38;
Matches 88; Conservative 19; Mismatches 9; Indels 6; Gaps 1;

Qy 1 QVQLQSGAEELVRPQTSVKVSKKASGYFTNLYLIEWVKRQPGQGLEWIGVINPGSGGTNY 60
   :|||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
Db 1 EVKLOESGPELVKPGASVKMSCKASGYFTSVVHHVRQKPGQGLDWIGYINPYNDGTDY 60
   :|||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|

Qy 61 NEKFGKATLTADKSSSTAYMOLSSLTSDSAVYFCARD-----GPFAYWGQGTTLTV 114
   :|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
Db 61 DEKFGKATLTSDKSSSTAYMELSSLTSDSAVYVYVYVYVYVYVYVYVYVYVYVYVY 120
   :|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|

Qy 115 SA 116
Db 121 SS 122

RESULT 14
US-08-392-419-2
; Sequence 2, Application US/08392419
; Patent No. 5624659
; GENERAL INFORMATION:
; APPLICANT: Bigner, Darell D.
; APPLICANT: Zalutsky, Michael R.
; TITLE OF INVENTION: METHOD OF TREATMENT
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 5624659th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/392,419
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/033,827
; FILING DATE: 19-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5405-90
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-392-419-2

Query Match      78.2%; Score 480; DB 1; Length 137;
Best Local Similarity 77.1%; Pred. No. 3.6e-38;
Matches 91; Conservative 12; Mismatches 13; Indels 2; Gaps 1;

Qy 1 QVQLQSGAEELVRPQTSVKVSKKASGYFTNLYLIEWVKRQPGQGLEWIGVINPGSGGTNY 60
   :|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
Db 20 EVQLQSGPELVKPGASVKMSCKASGYFTSVVHHVRQKPNQPGQGLEWIGYINPFNDGTY 79
   :|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|

Qy 61 NEKFGKATLTADKSSSTAYMOLSSLTSDSAVYFCARD--GPFAYWGQGTTLTVSA 116
   |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
Db 80 NEKFGKATLTSDRSSSTAYMELSSLTSESAVYFCARDMGREGPAYWGQGTTLTVSA 137
   |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
```

```
RESULT 15
US-08-497-312-15
; Sequence 15, Application US/08497312
; Patent No. 5712120
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Method for obtaining modified
; TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine
; TITLE OF INVENTION: antibody variable domains, compositions containing them.
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR
; STREET: 215 Y 15, ATABEY PLAYA
; CITY: HAVANA
; STATE:
; COUNTRY: CUBA
; ZIP: 11600
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/497,312
; FILING DATE: 30-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CU 80/94
; FILING DATE: 30-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BOND, LAURENCE B.
; REGISTRATION NUMBER: 30,549
; REFERENCE/DOCKET NUMBER: 2629US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 801/532-1922
; TELEFAX: 801/531-9168
; TELEX: 388961 1PM04UT
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
US-08-497-312-15
```

```
Query Match      77.9%; Score 478.5; DB 1; Length 123;
Best Local Similarity 74.0%; Pred. No. 4.5e-38;
Matches 91; Conservative 11; Mismatches 14; Indels 7; Gaps 1;

Qy 1 QVQLQSGAEELVRPQTSVKVSKKASGYFTNLYLIEWVKRQPGQGLEWIGVINPGSGGTNY 60
   :|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
Db 1 QVQLQSGAEELVRPQTSVKVSKKASGYFTNLYLIEWVKRQPGQGLEWIGVINPGSGGTNY 60
   :|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|

Qy 61 NEKFGKATLTADKSSSTAYMOLSSLTSDSAVYFCARDGPW-----FAYWGQGTTLV 113
   :|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
Db 61 NEKFGKATLTADKSSSTAYMOLSSLTSDSAVYVYVYVYVYVYVYVYVYVYVYVYVY 120
   :|||||  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|  |||:|

Qy 114 VSA 116
Db 121 VSS 123
```

Search completed: December 27, 2001, 09:03:06
Job time: 182 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2001, 09:00:04 ; Search time 25.84 Seconds
(without alignments)
341.960 Million cell updates/sec

Title: US-09-889-300A-1
Perfect score: 614
Sequence: 1 QVQLQSGAELVRPGTSVKV.....ARDGPWFAYWGQTLTVTSA 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	535.5	87.2	123	2 B30560	Ig heavy chain v r
2	526	85.7	123	2 S60067	Ig heavy chain v r
3	491.5	80.0	119	2 S20640	Ig heavy chain v r
4	491	80.0	135	2 A30577	Ig heavy chain pre
5	487.5	79.4	117	2 JC2269	PL7-6 antibody hea
6	487.5	79.4	119	2 C30562	Ig heavy chain v r
7	487	79.3	474	1 G2MS11	Ig gamma-2b chain
8	485	79.0	137	2 F29380	Ig heavy chain pre
9	484	78.8	118	2 C30560	Ig heavy chain v r
10	483.5	78.7	118	2 S38565	Ig heavy chain v r
11	483.5	78.7	138	2 S21810	Ig heavy chain v r
12	482.5	78.6	246	2 S38950	Ig gamma chain - m
13	482.5	78.6	446	2 S40295	Ig gamma-2a chain
14	481.5	78.4	119	2 E30562	Ig heavy chain v r
15	481	78.3	141	2 JL0076	Ig heavy chain pre
16	478.5	77.9	119	2 D30562	Ig heavy chain v r
17	478	77.9	137	2 E29380	Ig heavy chain pre
18	477.5	77.8	131	2 A27472	Ig heavy chain pre
19	476	77.5	140	2 S09216	Ig heavy chain pre
20	475.5	77.4	138	1 HVMS77	Ig heavy chain pre
21	475	77.4	115	2 A54378	Ig heavy chain v r
22	473.5	77.1	140	2 PH1482	Ig heavy chain v r
23	472.5	77.0	118	2 PL0231	Ig heavy chain v r
24	470	76.5	119	2 A24672	Ig heavy chain pre
25	469.5	76.5	117	2 S19566	Ig heavy chain v r
26	469.5	76.5	140	1 HVMSG7	Ig heavy chain pre
27	468	76.2	116	2 S09962	Ig heavy chain v-D
28	468	76.2	116	2 S53751	antibody Fab Jel 1
29	467.5	76.1	123	2 E48677	Ig heavy chain v-D

ALIGNMENTS

RESULT 1
B30560
Ig heavy chain V region (28.4.10A) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 23-Jul-1999
C:Accession: B30560
R:Matsuda, T.; Kabat, E.A.
J. Immunol. 142, 863-870, 1989
A:Title: Variable region cDNA sequences and antigen binding specificity of mouse mono
A:Reference number: A30560; MUID:89110062
A:Accession: B30560
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-123 <MAT>
A:Cross-references: GB:M24269; NID:g195619; PIDN:AAA38373.1; PID:g195620
C:Superfamily: immunoglobulin V region: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.2%; Score 535.5; DB 2; Length 123;
Best Local Similarity 87.8%; Pred. No. 1e-41;
Matches 108; Conservative 1; Mismatches 7; Indels 7; Gaps 2;

Qy 1 QVQLQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKRPGQGLEWIGVINPGSGGTNY 60
Db 1 QVQLQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKRQGLQDLEWIGVINPGSGGTNY 60
Qy 61 NEKFKGRATLTADKSSSFAYMQLSLLTSDDSAVYFCAR-----DGPW-FAYWGQGLT 113
Db 61 NEKFKGRATLTADKSSSFAYMQLSLLTSDDSAVYFCARSPDYDGYWYFDWGAGTTVT 120
Qy 114 VSA 116
Db 121 VSS 123

RESULT 2
S60067
Ig heavy chain V region (monoclonal antibody C3, gamma 2A) [validated] - mouse (fragm
C:Species: Mus musculus (house mouse)
C:Date: 23-Feb-1996 #sequence_revision 10-Oct-1997 #text_change 23-Mar-2001
C:Accession: S60067
R:Wien, M.W.; Filman, D.J.; Stura, E.A.; Gulllot, S.; Delpeyroux, F.; Crainic, R.; Ho
Nat. Struct. Biol. 2, 232-243, 1995
A:Title: Structure of the complex between the fab fragment of a neutralizing antibody
A:Reference number: S60066; MUID:95292109
A:Accession: S60067
A:Molecule type: mRNA
A:Residues: 1-123 <WIE>
A:Cross-references: EMBL:X84698; NID:g773225

R;Wien, M.W.; Hogle, J.M.
submitted to the Brookhaven Protein Data Bank, January 1995

A:Reference number: A52979; PDB:1FPT

C:Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 1-123

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin; pyroglutamic acid

F:15-98/Domain: immunoglobulin homology <IMM>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted

F:22-96/disulfide bonds: #status experimental

Query Match 85.7%; Score 526; DB 2; Length 123;
Best Local Similarity 85.0%; Pred. No. 7.5e-41;
Matches 102; Conservative 5; Mismatches 9; Indels 4; Gaps 1;

QY 1 QVQLQSGAELVPRGTSVKVSKASGYAFTNYLIIEWVKORPGGLEWIGVINPGSGGTNY 60

Db 1 QVQLQSGAELVPRGTSVKVSKASGYAFTNYLIQIKORPGGLEWIGVINPGSGGTDY 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARD---GPFAYWGQGLTLTVSA 116

Db 61 NANFKGKATLTADKSSSIYVQLSSLTSDSAVYFCARDFYDVGFDYWGQGLTLTVSS 120

RESULT 3

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C:Accession: S20640; S20644

R:Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.

submitted to the EMBL Data Library, February 1992

A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice react

A:Reference number: S20639

A:Accession: S20640

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-119 <LOS>

A:Cross-references: EMBL:X65002; NID:g52600; PIDN:CAA46135.1; PID:g52601; EMBL:X64999; N

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 491.5; DB 2; Length 119;
Best Local Similarity 77.3%; Pred. No. 9.6e-38;
Matches 92; Conservative 13; Mismatches 11; Indels 3; Gaps 1;

QY 1 QVQLQSGAELVPRGTSVKVSKASGYAFTNYLIIEWVKORPGGLEWIGVINPGSGGTNY 60

Db 1 EVQLQSGPELVKPGASVKMSCKASGYTFTSYVHWKQKPGRGLEWIGVINPDGSKY 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCAR---DGPWFAYWGQGLTLTVSA 116

Db 61 NEMFKGKATLTSDKSSSTAYMELSSLTSDSAVYFCARRATKGSWFAWYWGQGLTLTVSA 119

RESULT 4

A30577

Ig heavy chain precursor V region (MRL10) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 04-May-1989 #sequence_revision 04-May-1989 #text_change 16-Aug-1996

C:Accession: A30577

R:Kofler, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Theof

J.; Exp. Med. 161, 805-815, 1985

A:title: Genetic elements used for a murine lupus anti-DNA autoantibody are closely rela

A:Reference number: A30577; MUID:85159423

A:Accession: A30577

A:Molecule type: mRNA

A:Residues: 1-135 <KOF>

A:Cross-references: GB:M37621

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 491; DB 2; Length 135;
Best Local Similarity 82.8%; Pred. No. 1.2e-37;
Matches 96; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVQLQSGAELVPRGTSVKVSKASGYAFTNYLIIEWVKORPGGLEWIGVINPGSGGTNY 60

Db 20 QVQLQSGAELVPRGTSVKVSKASGYTFTSYVHWKQKPGRGLEWIGVINPGSGSTNY 79

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDGPFAYWGQGLTLTVSA 116

Db 80 NEKFKSKATLTVDTSSTAYMQLSSLTSDSAVYCARLVGGFAYWGQGLTLTVSA 135

RESULT 5

JC2269

PL7-6 antibody heavy chain - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 07-May-1999

C:Accession: JC2269; PC2186

R:Kurume, T.; Katayama, M.; Murakami, K.; Hashino, K.; Kamihagi, K.; Yasumoto, M.; Ka

J. Biochem. 115, 608-614, 1994

A:title: Expression of recombinant mouse/human chimeric antibody specific to human GM

A:Reference number: JC2269; MUID:94334310

A:Accession: JC2269

A:Molecule type: mRNA

A:Residues: 1-117 <KUR>

A:Accession: PC2186

A:Molecule type: protein

A:Residues: 2-27 <KU2>

A:Experimental source: hybridoma cell

C:Comment: this protein is specific to human P-selectin.

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:2-98/Region: V segment

F:15-98/Domain: immunoglobulin homology <IMM>

F:99-106/Region: D segment

F:107-117/Region: J segment

Query Match 79.4%; Score 487.5; DB 2; Length 117;
Best Local Similarity 78.6%; Pred. No. 2.2e-37;
Matches 92; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

QY 1 QVQLQSGAELVPRGTSVKVSKASGYAFTNYLIIEWVKORPGGLEWIGVINPGSGGTNY 60

Db 1 EVQLQSGAELVPRGTSVKVSKASGYTFTSYVHWKQKPGRGLEWIGVINPGTAYTEH 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDGP-WFAYWGQGLTLTVSA 116

Db 61 NOKFKDKATLTADKSSSTAYMQLSSLTSDSAVYCASGNPAWFAWYWGQGLTLTVSA 117

RESULT 6

C30562

Ig heavy chain V region (27.7.2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996

C:Accession: C30562

R:Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison,

J. Immunol. 142, 888-893, 1989

A:title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen

A:Reference number: A30562; MUID:89110066

A:Accession: C30562

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-119 <SIK>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-118 <MAT>
A:Cross-references: GB:M24270; NID:g195615; PIDN:AAA38371.1; PID:g195616
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 484; DB 2; Length 118;
Best Local Similarity 78.0%; Pred. No. 4.6e-37;
Matches 92; Conservative 10; Mismatches 14; Indels 2; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNLYIEWVKORPGGLEWIGVINPGSGGTNY 60

DB 1 QVHLQSGAELVRPGTSVKVSKASGYAFTNLYIEWVKORPGGLEWIGVINPGSGGTNY 60

QY 61 NEKFKGKATLTADKSSSTAYMOLSSLTSDSAVYFCAR--DGPWFAYWGQGLTVTVSA 116

DB 61 NOKFKKATLTVDKSSNTAYMOLSSLTSDSAVYFCARWGTSWFAYWGQGLTVTVSA 118

RESULT 10

S38565
Ig heavy chain V region (ASWV1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S38565

R:Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.

submitted to the EMBL Data Library, September 1993

A:Description: Molecular analysis of mercury-induced anti-nucleolar antibodies in H-2s M

A:Reference number: S38559

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-118 <MON>

A:Cross-references: EMBL:X75100; NID:g414157; PIDN:CAA52991.1; PID:g414158

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.7%; Score 483.5; DB 2; Length 118;
Best Local Similarity 78.8%; Pred. No. 5.1e-37;
Matches 93; Conservative 9; Mismatches 13; Indels 3; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNLYIEWVKORPGGLEWIGVINPGSGGTNY 60

DB 1 EVQLQSGAELVRAGSVKMSKASGYTFTSYGINWVKORPGGLEWIGVINPGNGYTKY 60

QY 61 NEKFKGKATLTADKSSSTAYMOLSSLTSDSAVYFCARDGP--WFAYWGQGLTVTVS 115

DB 61 NEKFKGKATLTVDKSSSTAYMQLRSLTSDSAVYFCAREGAGSYFYDYWGQGLTVTVS 118

RESULT 11

S21810

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C:Accession: S21810

R:Ostermeyer, M.; Brack, C.H.; Traunecker, A.; Koehler, G.

submitted to the EMBL Data Library, January 1991

A:Description: Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu heavy cha

A:Reference number: S21810

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-138 <OST>

A:Cross-references: EMBL:X56936; NID:g54163; PIDN:CAA40257.1; PID:g54164

C:Genetics:

A:Introns: 15/3

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 78.7%; Score 483.5; DB 2; Length 138;
Best Local Similarity 79.8%; Pred. No. 6e-37;
Matches 95; Conservative 7; Mismatches 14; Indels 3; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNLYIEWVKORPGGLEWIGVINPGSGGTNY 60

DB 20 QVQLQSGPELVKPGASVRIKSKASGYTFTSYIHWVKORPGGLEWIGIYPGNWTY 79

QY 61 NEKFKGKATLTADKSSSTAYMOLSSLTSDSAVYFCARD---GPFAYWGQGLTVTVSA 116

DB 80 NEKFKGKATLTADKSSSTAYMOLSSLTSDSAVYFCARNYSSYGLAYWGQGLTVTVSA 138

RESULT 12

S38950

Ig gamma chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999

C:Accession: S38950

R:Kleber, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.;

Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993

A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alp

A:Reference number: S38950; MUID:94128242

A:Accession: S38950

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-246 <KLE>

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 78.6%; Score 482.5; DB 2; Length 246;
Best Local Similarity 79.5%; Pred. No. 1.3e-36;
Matches 93; Conservative 7; Mismatches 16; Indels 1; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNLYIEWVKORPGGLEWIGVINPGSGGTNY 60

DB 1 QIQLQSGPELVKPGASVRIKSKASGYTFTDYIHWVKORPGGLEWIGIYPGSGNTKY 60

QY 61 NEKFKGKATLTADKSSSTAYMOLSSLTSDSAVYFCARDGPW-FAYWGQGLTVTVSA 116

DB 61 NEKFKGKATLTVDTSSTAYMQLSSLTSDSAVYFCARGKFAVDYWGQGSTVTSS 117

RESULT 13

S40295

Ig gamma-2a chain (mAb735) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999

C:Accession: S40295

R:Kleber, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.;

submitted to the EMBL Data Library, January 1993

A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 again

A:Reference number: S40295

A:Accession: S40295

A:Molecule type: protein

A:Residues: 1-446 <KLE>

C:Genetics:

A:Map position: 12

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid

F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>

F:1-117/Domain: V-D-J region <VDJ>

F:118-446/Domain: C region <CHR>

F:118-214/Domain: C1 region <CH1>

F:215-230/Region: hinge

F:231-340/Domain: C2 region <CH2>

F:341-446/Domain: C3 region <CH3>

F;297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match	78.3%;	Score 481;	DB 2;	Length 141;
Best Local Similarity	77.6%;	Pred. NO. 1e-36;		
Matches 90; Conservative	11;	Mismatches 15;	Indels	

Qy	1	OVOLQOAGALVRPGT	SVKVSCKASGYAFTN	LYLHWKQRP	GGGLEWIGVINPGSGGTNY	60
Db	20	QVOLQPGALVKPGASVKLS	ASGYTFTS	YWHHWKQRP	GGGLEWIGRIDPNSGGTKY	70
Qy	61	NEKFKGKATLTADKSS	YAMOLSSLTSDS	SAVYFCARDGP	FWFYAGQGTTLTVSA	116
Db	80	NEKFKSKATLTVDKPS	YAMOLSSLTSDS	SAVYFCAREGP	PAGDYGQGTTLTVSS	135

Search completed: December 27, 2001, 09:01:39
Job time: 95 sec

C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996

R; Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L. *J. Immunol.* 142, 888-893, 1989

A: Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-binding site
A: Reference number: A30562; MUID:89110066

```
A:Accession: E30562
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SIK>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      78.4%   Score 481.5; DB 2; Length 119;
Best Local Similarity 78.2%; Pred. No. 7.7e-37;
Matches 93; Conservative 9; Mismatches 14; Indels 3; Gaps

QY    1 QVQLQSGLLVRPCTSYKVSKASGYAFNYLIENWKQRPGGLEWIGVINPGSGCTNY 60
      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db     1 QVQLQSGLHLPQASKVKISCKATGTFSSWIEWWKQRPGHGLEWIGEIPFGSGSTKY 60

QY    61 NKFKGKATLTADKSSSTAYYMOLSSLTSDDSAVYFCAR--DGPWFAYWGQGTFLVTVA 116
      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db     61 NKFKGKATFTADTSNTFYAMOLSSLTSEDSAVYCARHYVGSSSFAYWGQGTFLVTVA 119
```

Query Match	78.4%;	Score 481.5;	DB 2;	Length 119;
Best Local Similarity	78.2%;	Pred. No. 7.7e-37;		
Matches 93; Conservative	9;	Mismatches 14;	Indels 3;	Gaps 1;

[illegible]

Qy	61	NEKFKGKATLTADKSSSTAYMOLSSLTSDDSAVYFCAR---	DGPWFAYWGQGLVTVSA	116
		: : :		
Db	61	NEKFKGKATFTADTSSNTAYMOLSSLTSEDSAVYCARHYGSSSFAYWGQGLVTVSA	119	

RESULT 15
JL0076
Ig heavy chain precursor V region (anti-phenylloxazolone, 18c10) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999

C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999

C;Accession: JL0076
P.Kaartinen M : Pöccä-Serra T : Mäkelä O

K. KADICINEN, M.: KOCCA SELLA, J., MAEKELAE, O.
Mol. Immunol. 25, 859-865, 1988

A;Title: Combinatorial association of V genes: one VH gene codes for three non-cross-reactive V genes
A;Reference number: JI0076; MUID:89096973

A; Accession: JL0076

A; MOLECULE TYPE: mRNA
A; Residues: 1-141 <KAA>

A;Cross-references: GB:M27788; NID:g195851; PIDN:AAA38441.1; PID:g195852

C;superfamily: immunoglobulin V region; immunoglobulin homology
C;keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F:20-141/Product: Ig heavy chain #status predicted <MAT>
F:34-117/Domain: immunoglobulin homolog <IMM>

F; 50-54/Region: complementarity-determining 1

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2001, 09:00:04 ; Search time 14.63 Seconds
(without alignments)
290.712 Million cell updates/sec

Title: US-09-889-300A-1
Sequence: 1 QVQLQSGAELVRPGTSVKV.....ARDGPWFAYWGQGLTVTVSA 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	475.5	77.4	138	1	HV48_MOUSE
2	471.5	76.8	120	1	HV03_MOUSE
3	469.5	76.5	140	1	HV02_MOUSE
4	466	75.9	139	1	HV07_MOUSE
5	457	74.4	137	1	HV11_MOUSE
6	455.5	74.2	117	1	HV12_MOUSE
7	454.5	74.0	117	1	HV13_MOUSE
8	454.5	74.0	121	1	HV01_MOUSE
9	432	70.4	120	1	HV05_MOUSE
10	429	69.9	117	1	HV04_MOUSE
11	427	69.5	117	1	HV02_MOUSE
12	425	69.2	118	1	HV51_MOUSE
13	414	67.4	117	1	HV06_MOUSE
14	414	67.4	117	1	HV09_MOUSE
15	411	66.9	117	1	HV05_MOUSE
16	411	66.9	117	1	HV49_MOUSE
17	410	66.8	117	1	HV10_MOUSE
18	401.5	65.4	136	1	HV15_MOUSE
19	385	62.7	147	1	HV1C_HUMAN
20	384	62.5	117	1	HV15_MOUSE
21	368	59.9	117	1	HV1G_HUMAN
22	363	59.1	117	1	HV1B_HUMAN
23	356	58.0	114	1	HV00_MOUSE
24	332.5	54.2	117	1	HV1A_HUMAN
25	327	53.3	122	1	HV3G_HUMAN
26	324	52.8	119	1	HV37_MOUSE
27	320	52.1	119	1	HV40_MOUSE
28	316.5	51.5	121	1	HV3J_HUMAN
29	316	51.5	120	1	HV1H_HUMAN
30	314.5	51.2	142	1	HV01_RAT
31	312	50.8	119	1	HV38_MOUSE
32	309.5	50.4	119	1	HV3I_HUMAN
33	308.5	50.2	115	1	HV32_MOUSE

34	308.5	50.2	117	1	HV17_MOUSE	P01786 mus musculu
35	308.5	50.2	117	1	HV41_MOUSE	P01811 mus musculu
36	308.5	50.2	125	1	HV1F_HUMAN	P06326 homo sapien
37	305.5	49.8	117	1	HV42_MOUSE	P01812 mus musculu
38	304.5	49.6	118	1	HV39_MOUSE	P01809 mus musculu
39	303.5	49.4	113	1	HV30_MOUSE	P01799 mus musculu
40	303	49.3	136	1	HV16_MOUSE	P01783 mus musculu
41	301	49.0	126	1	HV3K_HUMAN	P01772 homo sapien
42	300.5	48.9	115	1	HV33_MOUSE	P01802 mus musculu
43	299	48.7	114	1	HV01_CANFA	P01784 canis famil
44	299	48.7	114	1	HV3B_HUMAN	P01763 homo sapien
45	298.5	48.6	113	1	HV27_MOUSE	P01796 mus musculu

ALIGNMENTS

```
RESULT 1
HV48_MOUSE
ID HV48_MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
delta in an IgD-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR; A02033; HVNST7.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR SMART; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 128 138 FRAMEWORK 4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;
```

Query Match 77.48; Score 475.5; DB 1; Length 138;
Best Local Similarity 77.3%; Pred. No. 7.5e-42;
Matches 92; Conservative 8; Mismatches 16; Indels 3; Gaps 2;

```
Qy 1 QVQLQSGAELVRPGTSVKVSKASGAYFTNLYLEWKQRPQGGLWVTPGSGGTNY 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 20 QVQLQSGAELVRPGTSVKVSKASGAYFTNLYLEWKQRPQGGLWVTPGSGGTNY 79
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSSAVYFCAR-DG--PWFAYWGQGLTVTVSA 116
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 NEKFKKATLTVDKSSSTAYMQLSSLTPEEFAYVYCARSDGYDWFYWGQGLTVTVSA 138
```

RESULT 2
HV03_MOUSE STANDARD; PRT; 120 AA.
ID HV03_MOUSE

```
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsonate
RT idotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
DR PIR; A02028; HVMSG7.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
FT NON_TER 120 120
FT SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;
SQ

Query Match 76.8%; Score 471.5; DB 1; Length 120;
Best Local Similarity 76.7%; Pred. No. 1.6e-41;
Matches 92; Conservative 8; Mismatches 15; Indels 5; Gaps 1;

QY 2 VQLQSGAELVRPGTSVKVSKASGYAFNTYLIIEWVKQPGGLEWIGVINPGSGGTNYN 61
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 VQLQSGAELVRAGSSVKMSKASGYTFTSYGINVWKQPGGLEWIGVINPGNGYTKYN 60

QY 62 EKPKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARD-----GPMFAYWGQGLTVTVA 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 EKPKGKATLTVDKSSSTAYMQLRSLTSDSAVYFCARSYVYGGSYDFDYWGQGLTVTVA 120

RESULT 3
HV02_MOUSE
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 93G7 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A/J;
RC MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
```

```
CC -----
DR EMBL; J00493; AAA38128.1; -.
DR PIR; A02028; HVMSG7.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT NON_TER 140 140
FT SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;
SQ

Query Match 76.5%; Score 469.5; DB 1; Length 140;
Best Local Similarity 76.9%; Pred. No. 3.1e-41;
Matches 93; Conservative 9; Mismatches 14; Indels 5; Gaps 2;

QY 1'QVQLQSGAELVRPGTSVKVSKASGYAFNTYLIIEWVKQPGGLEWIGVINPGSGGTNY 60
   :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|
Db 20 EVQLQSGAELVRAGSSVKMSKASGYTFTSYGINVWKQPGGLEWIGVINPGNGYNY 79

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARD-----GPMFAYWGQGLTVTVA 115
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 NEKFKGKATLTVDKSSSTAYMQLRSLTSDSAVYFCARSYVYGGSYDFDYWGQGLTVTVA 139

QY 116 A 116
Db 140 S 140

RESULT 4
HV07_MOUSE
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RC MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; J00529; AAA38170.1; -.
DR PIR; A02034; MHMS18.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT
```

```
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match
Best Local Similarity 74.28; Score 466; DB 1; Length 139;
Matches 89; Conservative 11; Mismatches 16; Indels 4; Gaps 1;

Qy 1 QVQLQQSGAEILVRPGTSVKVSKCKASGYFTNYLIEWVKRPGQGLEWIGVINPGSGGTNY 60
Db 20 QVQLQQPGAEIVKPGASVKLCKCKASGYFTSYLMHWVNQRPGRGLEWIGRIDPNSGGTKY 79

Qy 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSSAVYFCAR---DGPWFAYWGQGLTVTVSA 116
Db 80 NEKFKSKATLTVDKPSSTAYMQLSLTSDSSAVYCYARYDYGGSYFDYWGQGLTLTVSS 139

RESULT 5
HV11_MOUSE
ID HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION S43 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J00539; AAA38172.1; -.
CC PIR: A02038; G2MS43.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_v.
CC Pfam: PF00047; Ig; 1.
CC SMART: SM00406; Igv; 1.
CC Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 FRAMEWORK 3.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
```

```
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match
Best Local Similarity 74.4%; Score 457; DB 1; Length 137;
Matches 87; Conservative 12; Mismatches 17; Indels 2; Gaps 1;

Qy 1 QVQLQQSGAEILVRPGTSVKVSKCKASGYFTNYLIEWVKRPGQGLEWIGVINPGSGGTNY 60
Db 20 QVQLQQPGAEIVKPGASVKLCKCKASGYFTSYLMHWVNQRPGRGLEWIGRIDPNSGGTKY 79

Qy 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSSAVYFCARD--GPWFAYWGQGLTVTVSA 116
Db 80 NEHFRSKATLTIDKPSSTAYMQLSLTSDSSAVYCYARYRLGRYFDYWGQGLTLTVSS 137

RESULT 6
HV12_MOUSE
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC PIR: A02039; MIMS4E.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_v.
CC Pfam: PF00047; Ig; 1.
CC SMART: SM00406; Igv; 1.
CC Immunoglobulin V region; Glycoprotein.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match
Best Local Similarity 74.2%; Score 455.5; DB 1; Length 117;
Matches 86; Conservative 14; Mismatches 16; Indels 1; Gaps 1;

Qy 1 QVQLQQSGAEILVRPGTSVKVSKCKASGYFTNYLIEWVKRPGQGLEWIGVINPGSGGTNY 60
Db 1 EVQLQQSGPELVKPGASVKMCKCKASGYFTDYKMKWKQSHKSLWIGDINPNNGGTSY 60

Qy 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSSAVYFCARDGPW-FAYWGQGLTVTVSA 116
Db 61 NQKFKGKATLTVDKSSSTAYMQLSLTSDSSAVYCYARYDYFDYWGAGTGVTVVSS 117

RESULT 7
HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
```

```

Query Match          70.4%; Score 432; DB 1; Length 120;
Best Local Similarity 69.2%; Pred. No. 1.8e-37;
Matches 83; Conservative 13; Mismatches 20; Indels 4; Gaps

QY 1 QVQLQQSGAEIVRPGTISVKYSCRASGYAFNYLIEWVKRPGQGQGLEWIGVINPGSGCTNY 60
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1 QVQLQPQGTSLVRFQASVNLSCRASGYFTFSYWMHWIRQRPQGQGLEWIGGINPSGCTNY 60
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 61 NEKFKGKATLTADKSSSTAYTQWLSLTSDDSAVYFCAR---DGP-WFAYWGQGTFLVTVSA 118
      ||||| ||||| ||||| ||||| :||| :||| :||| :||| :||| :||| :|||
      ||||| ||||| ||||| ||||| :||| :||| :||| :||| :||| :||| :|||
Db 61 NEKFKSKATLTVDKSSSATYMQLSPTPSDSAVYCARWDYEGDRYFDVWVGTTGTVTVSS 120
      ||||| ||||| ||||| ||||| :||| :||| :||| :||| :||| :||| :|||

RESULT 10
HV04_MOUSE
ID HV04_MOUSE STANDARD; PRT; 117 AA.
AC P01748;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 23 PRECURSOR.

```

```
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Inanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR PIR: A02030; HVMS23.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 59 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 69.9%; Score 429; DB 1; Length 117;
Best Local Similarity 81.6%; Pred. No. 3.5e-37;
Matches 80; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

OY 1 QVQLQSGAEIVRPGTSVKVSKASGYAFTNYLIEMVKRPGQGLEWIGVINPGSGGTNY 60
DB 20 QVQLQPGTELKPGASVKLSCKASGYFTSYMHWVKRPGQGLEWIGNINPGNGGTNY 79

OY 61 NEKFKGKATLTADKSSSTAYMQLSLSLSDSDSAVYFCAR 98
DB 80 NEKFKSKVTLTVDKSSSTAYTQLSLSLSDSDSAVYFCAR 117

RESULT 11
HV52_MOUSE
ID HV52_MOUSE STANDARD; PRT: 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION VH558 A1/A4 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;
RA "Developmentally controlled and tissue-specific expression of
RT unrearranged VH gene segments.";
RL Cell 40:271-281(1985).

-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
```

```
CC EMBL; M13787; AAA38499.1; -.
DR PIR: A02029; HVMSA1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 59 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 69.5%; Score 427; DB 1; Length 117;
Best Local Similarity 83.7%; Pred. No. 5.7e-37;
Matches 82; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

OY 1 QVQLQSGAEIVRPGTSVKVSKASGYAFTNYLIEMVKRPGQGLEWIGVINPGSGGTNY 60
DB 20 QVQLQSGPELVKPGALVKISCKASGYFTSYDINWVKRPGQGLEWIGWIYPGGGSTRY 79

OY 61 NEKFKGKATLTADKSSSTAYMQLSLSLSDSDSAVYFCAR 98
DB 80 NEKFKGKATLTADKSSSTAYMQLSLSLSDSDSAVYFCAR 117

RESULT 12
HV51_MOUSE
ID HV51_MOUSE STANDARD; PRT: 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR: A02040; MHMS38.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 69.2%; Score 425; DB 1; Length 118;
Best Local Similarity 68.6%; Pred. No. 9.2e-37;
Matches 81; Conservative 14; Mismatches 21; Indels 2; Gaps 1;

OY 1 QVQLQSGAEIVRPGTSVKVSKASGYAFTNYLIEMVKRPGQGLEWIGVINPGSGGTNY 60
DB 1 EVQLQSGPELVKPGASVKISCKASGYFTTDYIMNWKQSHGKSLIEWIGDINPNNGGTSY 60
```

```
QY 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCARDGPW--FAYWGGCTLTWVSA 116
I:||||| 11111 11111 11111 11111 11111 11111 11111 11111 11111
Db 61 NQKFKGKATLTVDKSSSATWELSLTSDSAVYCYARGYDFFDWGCTTWTVSS 118

RESULT 13
HV06_MOUSE
ID HV06_MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 102 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC
CC PIR; A02032; HVM502.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 59 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12867 MW; 740A65D0851FCA8C CRC64;

Query Match 67.4%; Score 414; DB 1; Length 117;
Best Local Similarity 81.2%; Pred. No. 1.2e-35;
Matches 78; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 2 VQLQSGAELVRPCTSVKSKASGYAFTNYLIEWVKQPGGLEWGVNPGSGGTNYN 61
||||| 11111 11111 11111 11111 11111 11111 11111 11111 11111
Db 21 VQLQPGAELVKGASVKVSKASGYTFTSYWVHWVKQPGGLEWIGRIHPSDSTNYN 80

QY 62 EKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCA 97
:||||| 11111 11111 11111 11111 11111 11111 11111 11111
Db 81 QKFKGKATLTVDKSSSATWELSLTSDSAVYFCA 116

RESULT 14
HV09_MOUSE
ID HV09_MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 186-1 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC
CC PIR; B02034; HVM561.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 59 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12890 MW; 16191A08CB17F5A CRC64;

Query Match 67.4%; Score 414; DB 1; Length 117;
Best Local Similarity 79.6%; Pred. No. 1.2e-35;
Matches 78; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 QVLOQSGAELVRPGTSVKVSKASGYAFTNYLIEWVKQPGGLEWGVNPGSGGTNY 60
||||| 11111 11111 11111 11111 11111 11111 11111 11111 11111
Db 20 QVLOQPGAELVPGASVKLCKASGYTFTSYWVHWVKQPGGLEWIGRIDPNSGGTKY 79

QY 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCAR 98
||||| 11111 11111 11111 11111 11111 11111 11111 11111
Db 80 NEKFKGKATLTVDTSSTAYMQLSLTSDSAVYFCAR 117

RESULT 15
HV05_MOUSE
ID HV05_MOUSE STANDARD; PRT; 117 AA.
AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 3 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
```


THIS PAGE BLANK (USPTO)

GenCore version 4.5
 Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2001, 09:00:04 ; Search time 38.99 Seconds
 (without alignments)
 435.178 Million cell updates/sec

Title: US-09-889-300A-1
 Perfect score: 614
 Sequence: 1 QVQLQSGAELVFPCTSVKVV.....ARDGPFAYWGQGLTVTVA 116

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
 Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database :

SPTREMBL_17:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	526.5	85.7	473	11 Q9D8L4	Q9D8L4 mus musculus
2	477	77.7	463	11 Q9D8L4	Q9D8L4 mus musculus
3	458.5	74.7	117	11 Q9QXF0	Q9QXF0 mus musculus
4	457	74.4	118	11 Q9Z1C4	Q9Z1C4 mus musculus
5	453.5	73.9	117	11 Q9QXE9	Q9QXE9 mus musculus
6	453	73.8	473	11 Q9D8L4	Q9D8L4 mus musculus
7	449	73.1	109	11 Q9JL75	Q9JL75 mus musculus
8	435.5	70.9	117	11 Q9Z1C6	Q9Z1C6 mus musculus
9	429	69.9	110	11 Q9JL83	Q9JL83 mus musculus
10	422	68.7	111	11 Q9D9B8	Q9D9B8 mus musculus
11	415.5	67.7	119	4 Q9UL94	Q9UL94 homo sapien
12	411	66.9	110	11 Q9JL77	Q9JL77 mus musculus
13	406	66.1	114	11 Q9JL81	Q9JL81 mus musculus
14	404.5	65.9	468	11 Q9JL31	Q9JL31 mus musculus
15	404	65.8	124	4 Q9UL92	Q9UL92 homo sapien
16	403.5	65.7	125	4 Q9UL95	Q9UL95 homo sapien
17	402.5	65.6	119	5 Q9GZ22	Q9GZ22 schistosoma
18	373	60.7	116	4 Q9UL89	Q9UL89 homo sapien
19	367.5	59.9	157	4 Q95978	Q95978 homo sapien

RESULT	1	500	4	Q9BRV0	Q9brv0 homo sapien
Q9D8L4					
ID	Q9D8L4	59.0	109	11 Q9JL85	Q9JL85 mus musculus
AC	Q9D8L4	58.6	150	4 Q9Y298	Q9Y298 homo sapien
DT	01-JUN-2001 (TREMBLrel. 17, Created)	57.9	484	11 Q9JLA6	Q9JLA6 mus musculus
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)	53.5	298	11 Q9QYF0	Q9QYF0 mus musculus
DE	1810060009RIK PROTEIN.	53.4	102	11 Q9JL79	Q9JL79 mus musculus
GN	1810060009RIK	50.9	120	4 Q9BUA1	Q9BUA1 homo sapien
OS	Mus musculus (Mouse).	50.5	113	4 Q9UL90	Q9UL90 homo sapien
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	50.4	112	4 Q9HCC1	Q9HCC1 homo sapien
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	50.3	147	4 Q9Y509	Q9Y509 homo sapien
OX	NCBI_TaxID=10090;	50.2	116	4 Q9UL93	Q9UL93 homo sapien
RN	SEQUENCE FROM N.A.	50.0	487	11 Q99KA4	Q99KA4 mus musculus
RC	STRAIN=C57BL/6J; TISSUE=PANCREAS;	49.3	119	4 Q9UL73	Q9UL73 homo sapien
RX	MEDLINE=21085660; PubMed=11217851;	49.2	122	4 Q9UL84	Q9UL84 homo sapien
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,	49.0	124	6 Q9N0W6	Q9N0W6 cryptolaqus
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,	48.7	124	6 Q9N0W4	Q9N0W4 cryptolaqus
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,	48.5	131	4 Q9UL14	Q9UL14 mus musculus
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,	48.1	121	4 Q9UL71	Q9UL71 homo sapien
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,	47.3	131	4 Q9UL88	Q9UL88 homo sapien
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,	47.2	118	4 Q9UL91	Q9UL91 homo sapien
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,	47.1	479	11 Q99M22	Q99M22 mus musculus
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,	45.4	597	4 Q9BU10	Q9BU10 homo sapien
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,	45.1	121	11 Q99NG4	Q99NG4 mus musculus
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,	44.7	597	4 Q9BOB8	Q9BOB8 homo sapien
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,	44.5	112	4 Q9UGP3	Q9UGP3 homo sapien
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,				
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,				
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,				
RA	Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,				
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kotsuki S.,				
RA	Hayashizaki Y.;				
RL	*Functional annotation of a full-length mouse cdna collection.*;				
RL	Nature 409:685-690(2001).				
CC	-i- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX				
CC	DOMAIN.				
CC	EMBL; AK007918; BAB25349.1; -				
DR	MGD; MGI:1924014; 1810060009RIK.				
DR	InterPro; IPR003599; Ig.				

ALIGNMENTS

PRT; 473 AA.

```
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003600; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; ig; 4.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IGcl; 3.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00410; IG-like; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FB CRC64;

Query Match 85.7%; Score 526.5; DB 11; Length 473;
Best Local Similarity 84.9%; Pred. No. 2.1e-46;
Matches 101; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKKASGYAFNLYLIEWVKORPGGLEWIGVINPGSGGTNY 60
DB 20 QVQLQSGAELVRPGASVKISCKASGYTFDYINNVKORPGGLEWIGKIGPGSGSTY 79
QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDG---PWFAYWGQGLTVTVA 116
DB 80 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARSGYDYDFAYWGQGLTVTVA 138

RESULT 2
Q99LC4 PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1;
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6B8C30783 CRC64;

Query Match 77.7%; Score 477; DB 11; Length 463;
Best Local Similarity 77.5%; Pred. No. 2.7e-41;
Matches 93; Conservative 7; Mismatches 16; Indels 4; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKKASGYAFNLYLIEWVKORPGGLEWIGVINPGSGGTNY 60
DB 20 QVQLQSGAELARPGASVRLSKASGYTFGCVSVKORTGGGLEWGIYPGSGNTY 79
QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDGPW---FAYWGQGLTVTVA 116
DB 80 SEKFKGKATLTDDKSSSTAYMHLSSLTSDSAVYFCARSGYSYDLFAYWGQGLTVTVA 139

RESULT 3
Q9QXF0 PRELIMINARY; PRT; 117 AA.
AC Q9QXF0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RA Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN
DR EMBL; AJ225171; CAB65236.1;
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match 74.7%; Score 458.5; DB 11; Length 117;
Best Local Similarity 73.5%; Pred. No. 4.4e-40;
Matches 86; Conservative 16; Mismatches 14; Indels 1; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKKASGYAFNLYLIEWVKORPGGLEWIGVINPGSGGTNY 60
DB 1 EVQLQSGPELVKPGASVKMSCKASGYTFDYIMKVKVKGSHGKSLWIGDINPNNGTSY 60
QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDGP-WFAYWGQGLTVTVA 116
DB 61 NOKFKGKATLTVDKSSSTAYMQLNSLTSDSAVYFCARDKYDFYWGQGLTLTVSS 117

RESULT 4
Q9Z1C4 PRELIMINARY; PRT; 118 AA.
AC Q9Z1C4;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matis L.M., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT IgG2/G4 constant regions block human leukocyte binding to porcine
RT endothelial cells.";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN
DR EMBL; U78801; AAD00293.1;
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 13036 MW; 90EEC559D31EC4FC CRC64;

Query Match 74.4%; Score 457; DB 11; Length 118;
Best Local Similarity 73.7%; Pred. No. 6.4e-40;
Matches 87; Conservative 13; Mismatches 16; Indels 2; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKKASGYAFNLYLIEWVKORPGGLEWIGVINPGSGGTNY 60
DB 1 QVQVQSGAELARPGASVKLSCKASGYNFNSYMWQVKVORPGGLEWIGAIYFGDGTYSY 60
QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARD--GWFAFYWGQGLTVTVA 116
DB 61 TQKFRGKATLTADKSSSTAYMQLSLASEDSAVYFCARVTGCGYDFYWGQGLTLTVSS 118
```

```
RESULT 5
Q9QXE9 PRELIMINARY; PRT: 117 AA.
ID Q9QXE9
AC Q9QXE9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademakers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AJ225117; CAB65237.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF84D499734 CRC64;

Query Match 73.9%; Score 453.5; DB 11; Length 117;
Best Local Similarity 73.7%; Pred. No. 1.5e-39;
Matches 87; Conservative 16; Mismatches 12; Indels 3; Gaps 2;

Oy 1 QVQLQQSGAEIVRPGTSVKVSKASGYFTNYLIEWVKQRPQGLEWIGVINPGSGGTNY 60
Db 1 EVQLQQSGPELVKPGASVKMSCKSGYFTTDYMKWVKQSKGLEWIGDINPNNGGTSY 60

Oy 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCARDGPWFA--YWGQGTFLVTVSA 116
Db 1 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCARDGPWFA--YWGQGTFLVTVSS 117

RESULT 6
Q99L25 PRELIMINARY; PRT: 473 AA.
ID Q99L25
AC Q99L25;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC003888; AAH03888.1; -.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 73.8%; Score 453; DB 11; Length 473;
Best Local Similarity 71.0%; Pred. No. 8.5e-39;
Matches 88; Conservative 10; Mismatches 18; Indels 8; Gaps 1;

Oy 1 QVQLQQSGAEIVRPGTSVKVSKASGYFTNYLIEWVKQRPQGLEWIGVINPGSGGTNY 60
Db 20 QVQLQQSDAEIVKPGASVKISCKVSGYFTTDHTTHWVKQRPQGLEWIGYIYPRDGSFKY 79

Oy 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCARDGP-----WFAYWGQGTFLV 112
Db 80 NEKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCARDGP-----WFAYWGQGTFLV 139
```

```
Oy 113 TVSA 116
Db 140 TVSS 143

RESULT 7
Q9JL75 PRELIMINARY; PRT: 109 AA.
ID Q9JL75
AC Q9JL75;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF206031; AAF69329.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
FT NON_TER 1
FT NON_TER 109
FT NON_TER 109
SQ SEQUENCE 109 AA; 12118 MW; FF65E441BBF936A6 CRC64;

Query Match 73.1%; Score 449; DB 11; Length 109;
Best Local Similarity 76.1%; Pred. No. 3.9e-39;
Matches 83; Conservative 14; Mismatches 10; Indels 2; Gaps 1;

Oy 10 ELVRPGTSVKVSKASGYFTNYLIEWVKQRPQGLEWIGVINPGSGGTNYNEKPKGRAT 69
Db 1 ELVKPGASVKMSCKASGYFTTSYVHHVVKQRPQGLEWIGYINPDGTYNEKPKGRAT 60

Oy 70 LTADKSSSTAYMQLSLTSDSAVYFCARDGPW--FAYWGQGTFLVTVSA 116
Db 61 LTADKSSSTAYMQLSLTSDSAVYFCARDGPW--FAYWGQGTFLVTVSS 109

RESULT 8
Q9Z1C6 PRELIMINARY; PRT: 117 AA.
ID Q9Z1C6
AC Q9Z1C6;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ANTI-PORCINE VCAM MAB 2A2 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matis L.M., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
IG2/G4 constant regions block human leukocyte binding to porcine
endothelial cells.";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: U78799; AAD00291.1; -.

```

DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig: 1.
DR SMART: SM00406; IGV: 1.
FT NON_TER 1 117
FT NON_TER 117
SQ SEQUENCE 117 AA; 13122 MW; 4F65B193AFB77E5B CRC64;

Query Match 70.9%; Score 435.5; DB 11; Length 117;
Best Local Similarity 70.1%; Pred. No. 1.1e-37;
Matches 82; Conservative 13; Mismatches 21; Indels 1; Gaps 1;
QY 1 QVLOQSGAELVPRGTSVKVSKKASGYATFNLYLIEWVKORPGOGLEWIGVINPFGSGGTNY 60
DB 1 QVLOQSGPQLVRPGTSVKVSKKASGYATFNLYLIEWVKORPGOGLEWIGVINPFGSGGTNY 60
QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCAR-DGPFAYWGQGLTLVTVA 116
DB 61 NQRLDKAILTVDKSSNTAYMQFGPTSEDSAVYCTRGVSNFAYWGQGLTLVTVA 117

RESULT 9
Q9JL83 PRELIMINARY; PRT; 110 AA.
AC Q9JL83;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
EMBL: AF206023; AAF69321.1; -;
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig: 1.
DR SMART: SM00406; IGV: 1.
FT NON_TER 110 110
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 12052 MW; 84E6F2AD219AF95E CRC64;

Query Match 69.9%; Score 429; DB 11; Length 110;
Best Local Similarity 78.2%; Pred. No. 4.7e-37;
Matches 86; Conservative 4; Mismatches 16; Indels 4; Gaps 2;

QY 10 ELVPRGTSVKVSKKASGYATFNLYLIEWVKORPGOGLEWIGVINPFGSGGTNYNEKFKGKAT 69
DB 2 ELVKPGASVKISKASGYATFNLYLIEWVKORPGOGLEWIGVINPFGSGGTNYNEKFKGKAT 61
QY 70 LTADKSSSTAYMQLSSLTSDSAVYFCARDPW--FAYWGQGLTLVTVA 116
DB 62 LTADKSSSTAYMQLSSLTSDSAVYFCARSN-NDVRFAYWGQGLTLVTVA 110

RESULT 10
Q9D9B8 PRELIMINARY; PRT; 111 AA.
AC Q9D9B8;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE ADULT MALE TESTIS CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:1700110L11, FULL INSERT SEQUENCE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RC MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasai H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RA Nature 409:685-690(2001).
RL "Functional annotation of a full-length mouse cDNA collection."
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
EMBL: AK007163; BAB24877.1; -;
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig: 1.
DR SMART: SM00409; IGV: 1.
DR SMART: SM00406; IGV: 1.
DR SMART: SM00410; IG_Like: 1.
SQ SEQUENCE 111 AA; 11976 MW; 874DDF7BD98BD7B2 CRC64;

Query Match 68.7%; Score 422; DB 11; Length 111;
Best Local Similarity 82.7%; Pred. No. 2.5e-36;
Matches 81; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 QVLOQSGAELVPRGTSVKVSKKASGYATFNLYLIEWVKORPGOGLEWIGVINPFGSGGTNY 60
DB 7 QVLOQSGPQLVRPGTSVKVSKKASGYATFNLYLIEWVKORPGOGLEWIGVINPFGSGGTNY 66
QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCAR 98
DB 67 NGKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCAR 104

RESULT 11
Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98277139; PubMed=9614934;
RX Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

```
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF035020; AAD56256.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;

Query Match 67.7%; Score 415.5; DB 4; Length 119;
Best Local Similarity 66.4%; Pred. No. 1.3e-35;
Matches 79; Conservative 14; Mismatches 23; Indels 3; Gaps 1;

Qy 1 QVQLQSGAELVRPCTSVKVKSCASGYAFTNYLIEWVKRPGQGLEWIGVINPGSGGTNY 60
Db 1 EVLVESGAELVRPCTSVKVKSCASGYFTTGYMHVVRQAPGQGLEWGWNPNSWTTNY 60

Qy 61 NEKFKGKATLTADKSSSTAYMQLSLSLTSDDSAVYFCARDGP---WFAYWGQGLTLTVSA 116
Db 61 AOKFGKVTMTKDTISISTAYWELSLRSLSDDTAVYYCARGGGRGLWFDPWGQGLTLTVSS 119

RESULT 12
Q9JL77 PRELIMINARY; PRT; 110 AA.
AC Q9JL77;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF206029; AAF69327.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
FT NON_TER 1
FT NON_TER 110
SQ SEQUENCE 110 AA; 12138 MW; 2EDE81FB5862C9AF CRC64;

Query Match 66.9%; Score 411; DB 11; Length 110;
Best Local Similarity 74.1%; Pred. No. 3.4e-35;
Matches 80; Conservative 9; Mismatches 17; Indels 2; Gaps 1;

Qy 11 LVRPCTSVKVKSCASGYAFTNYLIEWVKRPGQGLEWIGVINPGSGGTNYNEKFKGKATL 70
Db 3 LVRPCASVKLSCKASGYFTTSWVHWAKRPGQGLEWIGEIHPSNGHTNYNEKFKGKATL 62

Qy 71 TADKSSSTAYMQLSLSLTSDDSAVYFCARDGPWFA--YWGQGLTLTVSA 116
Db 63 TVDRSSSTAYVDLSLSLTSDESDSAVYCARQRNRYAMDWGQGLTVTVSS 110
```

```
RESULT 13
Q9JL81 PRELIMINARY; PRT; 114 AA.
AC Q9JL81;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF206025; AAF69323.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
FT NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 12829 MW; 404885FDE6BA56F8 CRC64;

Query Match 66.1%; Score 406; DB 11; Length 114;
Best Local Similarity 68.1%; Pred. No. 1.2e-34;
Matches 77; Conservative 13; Mismatches 17; Indels 6; Gaps 1;

Qy 10 ELVRPCTSVKVKSCASGYAFTNYLIEWVKRPGQGLEWIGVINPGSGGTNYNEKFKGKAT 69
Db 2 QLVRPGASVKISCKASGYFTSYMHVVKRPGQGLEWIGMIDPSDSETRLNQKFKDKAT 61

Qy 70 LTAKSSSTAYMQLSLSLTSDDSAVYFCARDG-----PWFAWVGQGLTLTVSA 116
Db 62 LTVDKSSSTAYMQLSPTSSESDSAVYCARSNYGSLSYFYDWGQGLTLTVSS 114

RESULT 14
Q9JL31 PRELIMINARY; PRT; 468 AA.
AC Q9JL31;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC003878; AAH03878.1; -.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B332ADB CRC64;

Query Match 65.9%; Score 404.5; DB 11; Length 468;
Best Local Similarity 64.7%; Pred. No. 8.7e-34;
Matches 77; Conservative 19; Mismatches 20; Indels 3; Gaps 1;

Qy 1 QVQLQSGAELVRPCTSVKVKSCASGYAFTNYLIEWVKRPGQGLEWIGVINPGSGGTNY 60
Db 20 EVQLQSGAELVRPGASVKLSCTASGFNIKDSLHWVVKRPGQGLEWIGWIDPEDGETKY 79

Qy 61 NEKFKGKATLTADKSSSTAYMQLSLSLTSDDSAVYFCARD---GPWFAYWGQGLTLTVSA 116
```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2001, 09:03:33 ; Search time 14.63 seconds
(without alignments)
268.157 Million cell updates/sec

Title: US-09-889-300A-2
Perfect score: 562
Sequence: 1 NIVMTQSPKSMMSVGRVT.....CGQGYSPYTFGGTKLEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 100059 seqs, 36664827 residues
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	562	100.0	136	1 KV5B_MOUSE	P01634 mus musculus
2	422	75.1	149	1 KV5A_MOUSE	P01633 mus musculus
3	403	71.7	114	1 KV1A_MOUSE	P01632 mus musculus
4	383	68.1	114	1 KV4A_HUMAN	P01625 homo sapien
5	376	66.9	134	1 KV4C_HUMAN	P06314 homo sapien
6	375	66.7	108	1 KV1M_HUMAN	P01605 homo sapien
7	370	65.8	108	1 KV1Y_HUMAN	P80362 homo sapien
8	365	64.9	108	1 KV1O_HUMAN	P01607 homo sapien
9	363	64.6	108	1 KV1V_HUMAN	P04430 homo sapien
10	362.5	64.5	133	1 KV4B_HUMAN	P06313 homo sapien
11	359	63.9	108	1 KV1H_HUMAN	P01600 homo sapien
12	359	63.9	111	1 KV3J_MOUSE	P01662 mus musculus
13	359	63.9	129	1 KV1X_HUMAN	P04432 homo sapien
14	358	63.7	108	1 KV1L_HUMAN	P01604 homo sapien
15	358	63.7	111	1 KV3H_MOUSE	P01660 mus musculus
16	358	63.7	129	1 KV1W_HUMAN	P04431 homo sapien
17	357	63.5	108	1 KV1N_HUMAN	P01606 homo sapien
18	356.5	63.4	129	1 KV3M_HUMAN	P18136 homo sapien
19	355.5	63.3	129	1 KV3L_HUMAN	P18135 homo sapien
20	354	63.0	131	1 KV3I_MOUSE	P01661 mus musculus
21	353	62.8	108	1 KV1E_HUMAN	P01597 homo sapien
22	353	62.8	111	1 KV3L_MOUSE	P01664 mus musculus
23	352.5	62.7	109	1 KV3B_HUMAN	P01620 homo sapien
24	352.5	62.7	109	1 KV3F_HUMAN	P01624 homo sapien
25	350	62.3	108	1 KV1A_HUMAN	P01593 homo sapien
26	349.5	62.2	109	1 KV3E_HUMAN	P01623 homo sapien
27	349	62.1	108	1 KV1K_HUMAN	P01603 homo sapien
28	349	62.1	108	1 KV1P_HUMAN	P01608 homo sapien
29	348	61.9	108	1 KV1B_HUMAN	P01594 homo sapien
30	348	61.9	108	1 KV1S_HUMAN	P01611 homo sapien
31	348	61.9	108	1 KV5M_MOUSE	P01646 mus musculus
32	347	61.7	108	1 KV1R_HUMAN	P01610 homo sapien
33	344.5	61.3	129	1 KV3H_HUMAN	P04207 homo sapien

34	343.5	61.1	109	1 KV3D_HUMAN	P01622 homo sapien
35	343	61.0	111	1 KV3K_MOUSE	P01663 mus musculus
36	342.5	60.9	113	1 KV2G_MOUSE	P01631 mus musculus
37	342	60.9	108	1 KV1G_HUMAN	P01599 homo sapien
38	342	60.9	108	1 KV1Q_HUMAN	P01609 homo sapien
39	342	60.9	108	1 KV5U_MOUSE	P04946 mus musculus
40	342	60.9	111	1 KV3M_MOUSE	P01665 mus musculus
41	341	60.7	108	1 KV1C_HUMAN	P01595 homo sapien
42	341	60.7	108	1 KV5K_MOUSE	P01644 mus musculus
43	339.5	60.4	108	1 KV3A_HUMAN	P01619 homo sapien
44	339	60.3	111	1 KV3D_MOUSE	P03977 mus musculus
45	339	60.3	111	1 KV3O_MOUSE	P01667 mus musculus

ALIGNMENTS

```

RESULT      1
KV5B_MOUSE
ID   KV5B_MOUSE          STANDARD;          PRT;   136 AA.
AC   P01634;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DE   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-V REGION MOPC 21 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82059477; PubMed=6170937;
RA   Hamlyn P.H., Gait M.J., Milstein C.;
RT   "Complete sequence of an immunoglobulin mRNA using specific priming
RT   and the dideoxynucleotide method of RNA sequencing.";
RL   Nucleic Acids Res. 9:4485-4494(1981).
RN   [2]
RP   SEQUENCE OF 30-136.
RX   MEDLINE=73054310; PubMed=4638343;
RA   Svastli J., Milstein C.;
RT   "The complete amino acid sequence of a mouse kappa light chain.";
RL   Biochem. J. 128:427-444(1972).
-----
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
-----
DR   EMBL: V00810; CAA24192.1; ALT_TERM.
DR   PIR: A01917; KVM521.
DR   InterPro: IPR003006; Ig_MHC.
DR   InterPro: IPR003596; Ig_V.
DR   Pfam: PF000047; Ig; 1.
DR   SMART: SM00406; IgV; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL              1
FT   CHAIN               29
FT   DOMAIN              30 136
FT   FRAMEWORK           1.
FT   COMPLEMENTARITY-DETERMINING 1.
FT   FRAMEWORK           2.
FT   COMPLEMENTARITY-DETERMINING 2.
FT   FRAMEWORK           3.
FT   COMPLEMENTARITY-DETERMINING 3.
FT   FRAMEWORK           4.
SQ   SEQUENCE 136 AA; 14902 MW; 8CDD85113996D1C2 CRC64;

```

Query Match 100.0%; Score 562; DB 1; Length 136;
Best Local Similarity 100.0%; Pred. No. 8.9e-54;

```

FT REPEAT      26      35
FT REPEAT     38      47
FT NON_TER    149     149
SQ SEQUENCE   149 AA; 16434 MW; B0480C87B682AC3E CRC64;

Query Match
Best Local Similarity 75.1%; Score 422; DB 1; Length 149;
Matches 84; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMNSVGRVTLTCKASENVVTVYSWYOOKPEOSPKLLIYGASNRYTGVDP 60
DB 42 DIVMTQSHKFMSTSVGRDVSITCKASODSSTVAWYOQPGQSPKLLIYSASYRTGVDP 101
QY 61 RFTGSGSATDFTLTSSVQAEDLADYHCGOGYSYPYTFGGGTGLEIK 107
DB 102 RFTGSGSGTDFTLTSSVQAEDLAHYVCQHYSPTPFTFGGTGLEIK 148

RESULT 3
KVIA_MOUSE STANDARD; PRT; 114 AA.
AC P01632;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION S107A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX MEDLINE=61241357; PubMed=6788890;
RP SEQUENCE FROM N.A.
RX Kwan S.-P., Rudikoff S., Seidman J.G., Leder P., Scharff M.D.;
RT "Nucleic acid and protein sequences of phosphocholine-binding light
RL chains."
RJ J. Exp. Med. 153:1366-1370(1981).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U29423; AAC00033.1; -.
DR PIR; A01915; KVMS7A.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 23
FT FT DOMAIN 24 40
FT FT DOMAIN 41 55
FT FT DOMAIN 56 62
FT FT DOMAIN 63 94
FT FT DOMAIN 95 103
FT FT DOMAIN 104 113
FT FT DISULFID 23 94
FT FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12717 MW; 32008EC8E9DBE67B CRC64;

Query Match
Best Local Similarity 71.7%; Score 403; DB 1; Length 114;
Matches 76; Conservative 16; Mismatches 15; Indels 6; Gaps 1;

QY 1 NIVMTQSPKSMNSVGRVTLTCKASENV-----VTYVSNYQQPESPKLLIYGASN 54

```



```
Db 1 DIVMTQSPTEFLAVTAKKVTISCTASELSYSSKHKVHVLAWYQKPEQSPKLLIYGASNR 60
QY 55 YTGVPDRFTGSGSATDFTLTITSSVOAEDLADYHCGQGYSPYPTFGGKLEIK 107
Db 61 YIGVDPDRFTGSGSGTDFTLTITSSVOQEDLTHYCAQFYSPYPLTFGAGTKLEIK 113

RESULT 4
KV4A_HUMAN
ID KV4A_HUMAN STANDARD; PRT; 114 AA.
AC P01625;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-IV REGION LEN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76004342; PubMed=50995;
RA Schneider M., Hilschmann N.;
RT "The primary structure of a monoclonic immunoglobulin-L-chain of
RT subgroup IV of the kappa type (Bence-Jones protein Len.).";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
RN [2]
RP REVISION TO 9.
RA Salomon A.;
RL Submitted (AUG-1996) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01903; K4HUL.
DR HSSP: P01789; 2MCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 40
FT DOMAIN 41 55
FT DOMAIN 56 62
FT DOMAIN 63 94
FT DOMAIN 95 101
FT DOMAIN 102 113
FT DISULFID 23 94
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;

Query Match 68.18; Score 383; DB 1; Length 114;
Best Local Similarity 65.58; Pred. No. 1.5e-34;
Matches 74; Conservative 18; Mismatches 15; Indels 6; Gaps 1;

QY 1 NIVMTQSPKSMVSGERVTLTCKASENVV-----TVVSWYQKPEQSPKLLIYGASNR 54
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIVMTQSPDSLAVSLGERATINCKSSQSYSSNKNYLAWYQKPGQPPKLLIYWASTR 60

QY 55 YTGVPDRFTGSGSATDFTLTITSSVOAEDLADYHCGQGYSPYPTFGGKLEIK 107
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ESGVDPDRFSGSGSGTDFTLTITSSLQAEDVAVYQYQYVLPWTFEGQGTKEIK 113

RESULT 5
KV4C_HUMAN
ID KV4C_HUMAN STANDARD; PRT; 134 AA.
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-IV REGION B17 PRECURSOR.
OS Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
SEQUENCE.
MEDLINE=77038198; PubMed=824717;

QY 1 NIVMTQSPKSMVSGERVTLTCKASENVV-----TVVSWYQKPEQSPKLLIYGASNR 54
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 DIVMTQSPDSLAVSLGERATINCKSSQSYSSNKNYLAWYQKPGQPPKLLIYWASTR 80

QY 55 YTGVPDRFTGSGSATDFTLTITSSVOAEDLADYHCGQGYSPYPTFGGKLEIK 107
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 81 ESGVDPDRFSGSGSGTDFTLTITSSLQAEDVAVYQYQYVLPWTFEGQGTKEIK 133

RESULT 6
KVIM_HUMAN
ID KVIM_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION LAY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
```

RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
RT IgM anti-gamma globulins (Lay/Pom) with shared idiotype
RT specificities";
RL Scand. J. Immunol. 5:677-684(1976).
CC -I- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01871; KIHULY.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT CONFLICT 30 31
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 66.7%; Score 375; DB 1; Length 108;
Best Local Similarity 65.4%; Pred. No. 1e-33;
Matches 70; Conservative 18; Mismatches 19; Indels 0; Gaps 0;
QY 1 NIWVTQSPKSMVSGVETLTCKASENVVTVYVSWYQKPEQSPKLLIYGASNRVYGVDP 60
DB 1 DIQMTQSPSLVSGVDRVTTCQASQNVNAYLNWYQKPGAPKLLIYGASTREAGVPS 60
QY 61 RFTGSGSATDFTLTSSVQAEADLYHCGQGYSPYTFGGGKLEIK 107
DB 61 RFGSGSGDTFTTSSLPEDIATYCCQYNNWPTFGGKVEVK 107

RESULT 7
KVLY_HUMAN STANDARD; PRT; 108 AA.
AC P80362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION WAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95086080; PubMed=7993911;
RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA Solomon A., Stevens F.J., Schiffer M.;
RT "Comparison of crystal structures of two homologous proteins:
RT structural origin of altered domain interactions in immunoglobulin
RT light-chain dimers";
RL Biochemistry 33:14848-14857(1994).
RN [2]
RP SEQUENCE OF 1-35.
RX MEDLINE=81267384; PubMed=6167731;
RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA Popp R.A., Solomon A.;
RT "Characterization and preliminary crystallographic data on the VL-
RT related fragment of the human Ki Bence Jones protein Wat.";
RL J. Mol. Biol. 147:185-193(1981).
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PDB; 1WTL; 01-NOV-94.

DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT BY SIMILARITY.
FT CONFLICT 30 31
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FA5697 CRC64;
Query Match 65.8%; Score 370; DB 1; Length 108;
Best Local Similarity 63.6%; Pred. No. 3.5e-33;
Matches 68; Conservative 20; Mismatches 19; Indels 0; Gaps 0;
QY 1 NIWVTQSPKSMVSGVETLTCKASENVVTVYVSWYQKPEQSPKLLIYGASNRVYGVDP 60
DB 1 DIQMTQSPSLVSGVDRVTTCRASQDITVYVNWYQKPGAPKLLIYGASILETGVP 60
QY 61 RFTGSGSATDFTLTSSVQAEADLYHCGQGYSPYTFGGGKLEIK 107
DB 61 RFGSGSGDTFTTSSLPEDIATYCCQYDTLTLTGGGKVDIK 107
RESULT 8
KVLO_HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION REI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup 1 (Bence-Jones protein Re1.); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL Biochemistry 14:4943-4952(1975).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01873; KIHURE.
DR PDB; IREI; 17-FEB-84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT BY SIMILARITY.
FT CONFLICT 30 31
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FA5697 CRC64;

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION ABPC 22/PC 9245.
OS Mus musculus (Mouse).

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

```
DR EMBL; X00966; CAA25478.1; ALT_TERM.  
DR PIR; A01884; K1HUDI.  
DR HSSP; P80362; 1WTL.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig_1.  
DR SMART; SM00406; Igv; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 22  
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION DAUDI.  
FT DOMAIN 23 45  
FT DOMAIN 23 45  
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 57 71 FRAMEWORK 2.  
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 79 110 FRAMEWORK 3.  
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING 3.  
FT DOMAIN 120 129 FRAMEWORK 4.  
FT DISULFID 45 110 BY SIMILARITY.  
FT NON_TER 129 129  
SQ SEQUENCE 129 AA; 14235 MW; CAF076BC7E5574C8 CRC64;  
  
Query Match 63.9%; Score 359; DB 1; Length 129;  
Best Local Similarity 59.8%; Pred. No. 6.6e-32;  
Matches 64; Conservative 19; Mismatches 24; Indels 0; Gaps 0;  
  
QY 1 NIVMTQSPKSMMSYGERVLTCTKASENVVTVVSWYQQRPEQSPKLLIYGASNRVTGVPD 60  
Db 23 DIQMTQSPSSLSASGDRVTITCRAGHNITNFSWYQQRPGKAPRLIIYAVSNLQVGVP 82  
  
QY 61 RFTGSGSATDFTLTSSVOAEDLADYHCGQGYSPYTFGGGKLEIK 107  
Db 83 RFTGSGSATDFTLTSSVOAEDLADYHCGQGYSPYTFGGGKLEIK 107  
  
RESULT 14  
KVIL_HUMAN STANDARD; PRT; 108 AA.  
AC P01604;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-I REGION KUE.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=79237924; PubMed=112021;  
RA Eulitz M., Kley H.-P., Zeitler H.-J.;  
RT "The primary structure of the Bence-Jones protein Kue. The amino acid  
sequence of the variable part of a human L-chain of the kappa-type.";  
RL Hope-Seyler's Z. Physiol. Chem. 360:725-734(1979).  
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
DR PIR; A01870; K1HUKU.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Igv; 1.  
DR SMART; SM00406; Igv; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23  
FT DOMAIN 24 34 FRAMEWORK 1.  
FT DOMAIN 35 49 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 50 56 FRAMEWORK 2.  
FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 89 97 FRAMEWORK 3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
```

```
FT DOMAIN 98 107 FRAMEWORK 4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON_TER 108 108  
SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90E4E98 CRC64;  
  
Query Match 63.7%; Score 358; DB 1; Length 108;  
Best Local Similarity 61.7%; Pred. No. 6.9e-32;  
Matches 66; Conservative 20; Mismatches 21; Indels 0; Gaps 0;  
  
QY 1 NIVMTQSPKSMMSYGERVLTCTKASENVVTVVSWYQQRPEQSPKLLIYGASNRVTGVPD 60  
Db 1 DIQMTQSPSTQPSASGDRVTITCRASQSIWLANVYQQRPEKAPKLLIYKASTLETGVP 60  
  
QY 61 RFTGSGSATDFTLTSSVOAEDLADYHCGQGYSPYTFGGGKLEIK 107  
Db 61 RFTGSGSATDFTLTSSVOAEDLADYHCGQGYSPYTFGGGKLEIK 107  
  
RESULT 15  
KV3H_MOUSE STANDARD; PRT; 111 AA.  
AC P01660;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-III REGION PC 3741/TEPC 111.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE (PC 3741).  
RX MEDLINE=79073152; PubMed=103003;  
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
RT "Rearrangement of genetic information may produce immunoglobulin  
RT diversity".  
RL Nature 276:785-790(1978).  
RN [2]  
RP SEQUENCE (TEPC 111).  
RX MEDLINE=79012520; PubMed=99744;  
RA McKean D.J., Bell M., Potter M.;  
RT "Mechanisms of antibody diversity: multiple genes encode structurally  
RT related mouse kappa variable regions".  
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).  
CC -!- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.  
DR PIR; A01934; KVMS37.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Igv; 1.  
DR SMART; SM00406; Igv; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 38 FRAMEWORK 1.  
FT DOMAIN 39 53 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 54 60 FRAMEWORK 2.  
FT DOMAIN 61 92 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 93 101 FRAMEWORK 3.  
FT DOMAIN 102 111 COMPLEMENTARITY-DETERMINING 3.  
FT DISULFID 23 92 BY SIMILARITY.  
FT NON_TER 111 111  
SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;  
  
Query Match 63.7%; Score 358; DB 1; Length 111;  
Best Local Similarity 61.3%; Pred. No. 7.1e-32;  
Matches 68; Conservative 21; Mismatches 18; Indels 4; Gaps 1;  
  
QY 1 NIVMTQSPKSMMSYGERVLTCTKASENVVTVVSWYQQRPEQSPKLLIYGASNRVT 56  
Db 1 DIIVTQSPASLAVSLGQRATISCRASEVDSYGNFMHWYQQRPGQPPKLLIYRASNLES 60  
  
QY 57 GVPDRFTGSGSATDFTLTSSVOAEDLADYHCGQGYSPYTFGGGKLEIK 107
```

Db 61 GIPARESGSRTDETLINPYEADVDATYCCQSNEDPYTEGGTKLEIK 111

Search completed: December 27, 2001, 09:03:33
Job time: 209 sec


```

DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 65.2%; Score 366.5; DB 4; Length 109;
Best Local Similarity 65.4%; Pred. No. 2.3e-32;
Matches 70; Conservative 20; Mismatches 16; Indels 1; Gaps 1;

QY 2 IVMTQSPKSMNSVGERVTLTCKASENV-VTVSVWQKPEQSPKLLIYGASNRVTGVPD 60
Db 2 IVLTQSPGTLSSLPGERATLSCRASQSVSSSYLAWYQKPGQAPRLIYGASSRATGIPD 61
[1]

QY 61 RTFGSGSATDFTLTISVQAEDLADYHCGQYSYPYTFGGGKLEIK 107
Db 62 RFSGSGSGDFTLTISRLEPEDCAVYCOQYGGSSPLTFGGGKVEIK 108

RESULT 4
QYER29 PRELIMINARY; PRT; 107 AA.
AC Q9ER29;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;
RT "Cloning and sequencing of the light chain fragment of variable region
RT genes of an anti-hTNF-a monoclonal antibody.";
RL J. Cell. Mol. Immunol. 12:21-26(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT "Construction and sequencing of the single-chain antibody gene of a
RT human TNF-alpha specific monoclonal antibody.";
RL Ti 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF262753; AAG23804.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 107
SQ SEQUENCE 107 AA; 11784 MW; 2B15EEA6604A26C3 CRC64;

Query Match 65.1%; Score 366; DB 11; Length 107;
Best Local Similarity 64.5%; Pred. No. 2.5e-32;
Matches 69; Conservative 17; Mismatches 15; Indels 6; Gaps 1;

QY 4 MTQSPKSMNSVGERVTLTCKASENV-----TVYSWYQKPEQSPKLLIYGASNRVTG 57
Db 1 MTQSPSLANSVGKVTMSCKSQSVLNSNTQKNYLAWYQKPGQPELVYFASTRSG 60
[1]

QY 58 VPDRTGSGSATDFTLTISVQAEDLADYHCGQYSYPYTFGGGKTKL 104
Db 61 VPDRTGSGSATDFTLTISVQAEDLADYHCGQYSYPYTFGGGKTKL 107

us-09-889-300a-2.rspt
```



```
RT fetus.;
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035044; AAD56280.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 1
FT SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 63.0%; Score 354; DB 4; Length 108;
Best Local Similarity 63.6%; Pred. No. 5.le-31;
Matches 68; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 NIWVTSQPSKMSVSGERVTLTKCKASENVVYVSWYQKPEQSPKLLIYGASNRVTGVPD 60
Db 1 DIQMTSPSLASVSDRVTTICRASQGISNLANWYQKPKVPSLIYAASLQSGVPS 60

QY 61 RFTGSGSATDFTLTISVQAEDLADYHCQGYSPYTFGGGKLEIK 107
Db 61 RFGSGSGTDFTLTISLQPEDVATYVCQKYNAPRTFGPGTKLEIK 107

RESULT 9
Q9UL81
ID Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035033; AAD56269.1; -.
DR HSP; P80362; IWL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 107
FT SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 62.5%; Score 351.5; DB 4; Length 107;
Best Local Similarity 61.7%; Pred. No. 9.5e-31;
Matches 66; Conservative 20; Mismatches 20; Indels 1; Gaps 1;

QY 1 NIWVTSQPSKMSVSGERVTLTKCKASENVVYVSWYQKPEQSPKLLIYGASNRVTGVPD 60
Db 1 DIQMTSPSLASVSDRVTTICRASQGISNLANWYQKPKAPNLLIYAASLQSGVPS 60

QY 61 RFTGSGSATDFTLTISVQAEDLADYHCQGYSPYTFGGGKLEIK 107
Db 61 RFGSGSGTDFTLTISLQQAEDPATYVCQGSY-ALTFPGTKVDIR 106
```

```
RESULT 10
Q9UL83
ID Q9UL83 PRELIMINARY; PRT; 108 AA.
AC Q9UL83;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035031; AAD56267.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 108
FT SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 61.7%; Score 347; DB 4; Length 108;
Best Local Similarity 61.3%; Pred. No. 2.9e-30;
Matches 65; Conservative 22; Mismatches 19; Indels 0; Gaps 0;

QY 2 IVWTSQPSKMSVSGERVTLTKCKASENVVYVSWYQKPEQSPKLLIYGASNRVTGVPD 61
Db 2 IVWTSQPSKMSVSGERVTLTKCKASENVVYVSWYQKPEQSPKLLIYGASNRVTGVPD 61

QY 62 FTGSGSATDFTLTISVQAEDLADYHCQGYSPYTFGGGKLEIK 107
Db 62 FSGSGSGTFTLTISLQPEDFAVYVCQHYNNWPFPGTKVDIK 107

RESULT 11
Q9UL86
ID Q9UL86 PRELIMINARY; PRT; 109 AA.
AC Q9UL86;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035028; AAD56264.1; -.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
```



```
SQ SEQUENCE 104 AA; 11360 MW; 5DA8BBFD5F0AA1AE CRC64;

Query Match 58.6%; Score 329.5; DB 11; Length 104;
Best Local Similarity 60.2%; Pred. No. 2.2e-28;
Matches 62; Conservative 18; Mismatches 18; Indels 5; Gaps 1;

QY 10 SMSMSYGERVTLTKASENVV-----TYSVSWQKPEQSPKLLIYGASNRYTGVPDRFTG 64
Db 2 SLPVSLGDQASISCRSSQSLVHTNGNTYLHWYLOKQSPKLLIYKYSNRFSGVDPDRFG 61

QY 65 SGSATDFTLTISVQAEADLYHCGQGYSPYTFGGGTKLEIK 107
Db 62 SSGGDTFTLKISRVEAEDLGVPFCSQTHVPYTFGGGTKLEIK 104

RESULT 15
Q9U410 PRELIMINARY; PRT; 106 AA.
AC Q9U410;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigeidida; Schistosomatidae; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the light chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF207620; AAF19434.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT 106
FT NON_TER 106
SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match 58.5%; Score 328.5; DB 5; Length 106;
Best Local Similarity 61.0%; Pred. No. 2.9e-28;
Matches 64; Conservative 16; Mismatches 24; Indels 1; Gaps 1;

QY 3 VMTQSPKMSMSYGERVTLTKASENVVTVSVWQKPEQSPKLLIYGASNRYTGVPDRF 62
Db 3 LLTQSPAIMASPGKVTMTCSASS--VSIVWYLOKPGSSPRLLIYDTSNLASGVPRF 61

QY 63 TGSGSATDFTLTISVQAEADLYHCGQGYSPYTFGGGTKLEIK 107
Db 62 SSGSGGTSYSLTISRMEADAATYCCQWTSPFTFGGSGTKLEIK 106

Search completed: December 27, 2001, 09:02:32
Job time: 148 sec
```

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2001, 09:01:00 ; Search time 41.13 Seconds
(without alignments)
192.702 Million cell updates/sec

Title: US-09-889-300A-2
Perfect score: 562
Sequence: 1 NIVMTQSPKMSMSVGERVT.....CCGQSYSPYTFGGTKLEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_1101.*
1: /SID52/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID52/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID52/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID52/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID52/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID52/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID52/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID52/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID52/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID52/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID52/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID52/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID52/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID52/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID52/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID52/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID52/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID52/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID52/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID52/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID52/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	562	100.0	107	19 AAW47086	Mouse J591 monoclonal
2	562	100.0	107	21 AAY90374	J591 monoclonal an
3	562	100.0	107	21 AAB10444	Murine monoclonal
4	562	100.0	107	22 AAB36225	Monoclonal antibod
5	562	100.0	109	13 AAR27144	IE6 kappa light ch
6	562	100.0	121	19 AAW47085	Mouse J591 monoclo
7	562	100.0	121	21 AAY90370	J591 monoclonal an
8	562	100.0	121	22 AAB36222	Murine monoclonal
9	562	100.0	127	17 AAW01145	MAB 10.1 light cha
10	527	93.8	136	17 AAW01632	Ber-H2 heavy kappa
11	521	92.7	127	21 AAY71545	Mouse AF2 antibody

12	521	92.7	136	22	AAB59693	Murine AF2 antibod
13	509	90.6	108	17	AAW00828	Variable light cha
14	482	85.8	239	16	AAW64812	ScFv anti-HCG. Mu
15	454	80.8	107	18	AAW21939	Variable light sub
16	454	80.8	107	20	AAV05271	Antibody 24-31 hum
17	449	79.9	107	20	AAV05269	Antibody 24-31 hum
18	449	79.9	133	18	AAW21934	Variable light sub
19	449	79.9	133	20	AAV05264	Antibody 24-31 hum
20	447	79.5	107	18	AAW21938	Variable light sub
21	447	79.5	107	20	AAV05270	Antibody 24-31 hum
22	447	79.5	133	18	AAW21936	Variable light sub
23	447	79.5	133	20	AAV05266	Antibody 24-31 hum
24	444	79.0	107	20	AAV05268	Antibody 24-31 hum
25	444	79.0	133	18	AAW21933	Variable light sub
26	444	79.0	133	20	AAV05263	Antibody 24-31 hum
27	441	78.5	107	13	AAW25731	Humanised VL regio
28	441	78.5	107	22	AAB69696	Human Eu antibody
29	441	78.5	128	21	AAV71547	Humanised antibody
30	432	76.9	108	21	AAB11392	Murine IIIF10 VL C
31	430	76.5	116	22	AAB67070	Murine G250 antibo
32	426	75.8	120	16	AAW74969	Anti-idiotypic anti
33	424.5	75.5	108	16	AAW82970	FB5 antibody light
34	423	75.3	107	20	AAW86140	Protein sequence o
35	423	75.3	108	19	AAW48863	Murine monoclonal
36	423	75.3	132	15	AAW48861	MAB A33 light chai
37	422	75.1	107	16	AAW74959	Immunoglobulin lig
38	422	75.1	131	19	AAW62187	Mouse anti-HM1.24
39	422	75.1	131	20	AAV02545	L chain V region o
40	422	75.1	237	20	AAW95440	A33/212 single-cha
41	422	75.1	237	21	AAV54836	Linked fusion prot
42	422	75.1	241	20	AAW95441	A33/218 single-cha
43	422	75.1	241	21	AAV54837	Linked fusion prot
44	422	75.1	245	20	AAW97891	A33/218 single cha
45	422	75.1	643	19	AAW73048	A33 chimeric recep

ALIGNMENTS

RESULT 1
AAW47086
ID AAW47086 standard; Protein; 107 AA.
XX AC AAW47086;
XX DT 26-JUN-1998 (first entry)
XX DE Mouse J591 monoclonal antibody light chain variable region
XX DE Mouse; monoclonal antibody; J591; prostate specific membrane antigen;
XX KW cancer; vascular endothelial cell; metastatic adenocarcinoma.
XX OS Mus sp.
XX PN W09803873-A1.
XX PD 29-JAN-1998
XX PF 17-JUL-1997; 97WO-US12035.
XX PR 09-APR-1997; 97US-0838682.
XX PR 18-JUL-1996; 96US-0022125.
(CORR) CORNELL RES FOUND INC.
Bander NH;
WPI: 1998-120937/11.
N-PSDB; AAV13952.
Destroying cancer cells with agent that binds to prostate specific membrane antigen - on vascular endothelial cells near the cancer, or on normal, hypertrophic or cancerous prostatic cells, also used for

PT diagnosis

PS Example 12; Page 60; 94pp; English.

XX The present sequence represents the mouse J591 monoclonal antibody light chain variable region from an example of the present invention. The present invention describes the elimination of cancer cells by treating cancer endothelial cells (VEC) close to the cancer with an agent (A) able to bind to the extracellular domain (ECD) of prostate specific membrane antigen (PSMA). (A) both binds to the VEC and destroys the cancer cells. Also described are: (1) the detection of cancer tissue by detecting binding of labelled (A) to VEC close to, or within, a cancer tissue; (2) eliminating or detecting normal, benignly hyperplastic or cancerous prostate epithelial cells using optionally labelled (A); (3) hybridomas that produce a monoclonal antibody (MAB) that binds to PSMA. The method is used to treat renal, urothelial, colon, lung, rectal or breast cancers and metastatic adenocarcinoma of the liver. The diagnostic method is particularly used to detect recurrence of prostatic disease or to monitor the effect of treatments for prostate cancer (presence of PSMA in the serum indicates that prostate cells are being lysed). (A) binds to an epitope of PSMA expressed on live cells (contrast antibody 7E11 which only binds after cell lysis), allowing targeting of live, unfixed cells and thus providing more efficient treatment and diagnosis. Both cancer cells themselves and the VEC on which they depend are killed. All VEC close to cancer cells express PSMA, whatever the type of cancer, but normal VEC do not.

XX Sequence 107 AA;

Query Match 100.0%; Score 562; DB 19; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.2e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIWMTQSPKMSMSVGERVTLTCKASENVVTVYVSWYQKPEQSPKLLIYGASNRVTGVPD 60
DB 1 NIWMTQSPKMSMSVGERVTLTCKASENVVTVYVSWYQKPEQSPKLLIYGASNRVTGVPD 60
QY 61 RFTGSGSATDFTLTISVQAEADLYHCQGYSYPYTFGGGKLEIK 107
DB 61 RFTGSGSATDFTLTISVQAEADLYHCQGYSYPYTFGGGKLEIK 107

RESULT 2
AAY90374
ID AAY90374 standard; Protein; 107 AA.
XX
AC AAY90374;
XX
DT 15-JAN-2001 (first entry)
XX
DE J591 monoclonal antibody light chain protein sequence fragment.

XX J591 monoclonal antibody; extracellular domain; diagnosis; therapy;
KW prostate specific membrane antigen; prostate cancer; light chain.
XX
OS Homo sapiens.
XX
PN US6107090-A.
XX
PD 22-AUG-2000.
XX
PF 09-APR-1997; 97US-0838682.
XX
PR 06-MAY-1996; 96US-0016976.
PR 18-JUL-1996; 96US-0022125.
XX
XX (CORR) CORNELL RES FOUND INC.
PA
XX Bander NH;
PI
XX WPI; 2000-571325/53.
DR N-PSDB; AAA37834.
XX

XX

PT Antibody specific for extracellular prostate-specific membrane antigen, useful for diagnosis and treatment of prostate cancer

XX Example 12; Column 22; 33pp; English.

XX This sequence is a fragment of the light chain of the monoclonal antibody J591. The invention relates to an isolated antibody or its antigen binding portion (I) which binds to an extracellular domain of prostate specific membrane antigen and which does not require cell lysis to bind to the extracellular domain. The antibody or its antigen binding portion is selected for its ability to bind to live cells. (I) is useful for diagnosis of diseases associated with the presence of normal, benign hyperplastic, and cancerous epithelial cells or portions. Also it can be used for identifying the recurrence of such diseases, particularly when the disease is localised in a particular biological material of the patient for e.g. recurrence of prostatic disease. They can also be used alone or bound to a substance effective to kill cancerous prostate epithelial cells as a therapy for prostate cancer. Binding and internalising of the antibody with the prostate specific membrane antigen, permits the therapeutic use of intracellularly acting cytotoxic agents. (I) targets only prostate epithelial cells and other tissue are spared which provides safer treatment particularly for elderly patients. The antibodies bind to living prostate cells and treatments using these antibodies are more effective than those which target lysed prostate cells.

XX Sequence 107 AA;

Query Match 100.0%; Score 562; DB 21; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.2e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIWMTQSPKMSMSVGERVTLTCKASENVVTVYVSWYQKPEQSPKLLIYGASNRVTGVPD 60
DB 1 NIWMTQSPKMSMSVGERVTLTCKASENVVTVYVSWYQKPEQSPKLLIYGASNRVTGVPD 60
QY 61 RFTGSGSATDFTLTISVQAEADLYHCQGYSYPYTFGGGKLEIK 107
DB 61 RFTGSGSATDFTLTISVQAEADLYHCQGYSYPYTFGGGKLEIK 107

RESULT 3
AAB10444
ID AAB10444 standard; protein; 107 AA.
XX
AC AAB10444;
XX
DT 01-DEC-2000 (first entry)
XX
DE Murine monoclonal antibody MAK HE2 variable region light chain.

XX Murine; monoclonal antibody; MAK HE2; light chain; variable region;
KW human cellular membrane antigen; tumor associated antigen; TAA;
KW vaccine; cancer.
XX
OS Mus sp.
XX
PN WO200041722-A1.
XX
PD 20-JUL-2000.
XX
PF 12-JAN-2000; 2000WO-EP00174.
XX
PR 13-JAN-1999; 99CH-0000051.
XX
XX (IGEN-) IGENEON GMBH.
XX
XX Eckert H, Loibner H;
XX
XX WPI; 2000-475956/41.
XX

PT Novel use of antibodies against human cellular membrane antigens for
 XX vaccination against cancer -
 PS Example 3; Page 47-48; 54pp; German.
 XX This invention describes the novel use of an antibody targeted to a
 CC human cellular membrane antigen, to manufacture a medicament to
 CC prophylactically and/or therapeutically vaccinate against cancer.
 CC The antibodies against tumor associated antigen (TAA) for prophylactic
 CC and/or therapeutic vaccination against cancer may be used in low doses
 CC (when compared to antibodies against TAA for passive immunotherapy),
 CC typically less than 1 mg by injection. The antibodies also have a long
 CC continual activity that directly induces immunity and their shelf life
 CC is unlimited (fresh vaccination is always possible). This sequence
 CC represents the murine monoclonal antibody MAX HE2 variable region light
 CC chain fragment which is used in the method of the invention.
 XX Sequence 107 AA;
 SQ

Query Match 100.0%; Score 562; DB 21; Length 107;
 Best Local Similarity 100.0%; Pred. No. 1.2e-39;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NIVMTQSPKSMVSGERVTLTKKASENVVTVSVYQOKPEQSPKLLIYGASNRVTGVPD 60
 Db 1 NIVMTQSPKSMVSGERVTLTKKASENVVTVSVYQOKPEQSPKLLIYGASNRVTGVPD 60
 Qy 61 RFTGSGSATDFTLTISVQAEDLADYHCGQGSYPYTFGGGKLEIK 107
 Db 61 RFTGSGSATDFTLTISVQAEDLADYHCGQGSYPYTFGGGKLEIK 107

RESULT 4
 AAB36225
 ID AAB36225 standard; Protein: 107 AA.
 AC AAB36225;
 XX
 DT 15-FEB-2001 (first entry)
 XX
 DE Monoclonal antibody J591 kappa light chain V region #1.
 XX
 KW Mouse; antibody; heavy chain; prostate cancer; biological agent.
 KW
 OS Mus sp.
 XX
 PN US6136311-A.
 XX
 PD 24-OCT-2000.
 XX
 PF 17-JUL-1997; 97US-0895914.
 XX
 PR 06-MAY-1996; 96US-0016976.
 PR 18-JUL-1996; 96US-0022125.
 PR 09-APR-1997; 97US-0838682.
 XX
 PA (CORR.) CORNELL RES FOUND INC.
 XX
 PI Bander NH;
 DR WPI: 2001-040234/05.
 DR N-PSDB; AAC66544.
 XX
 PT Use of E99, a J415, a J533 or a J591 monoclonal antibodies for ablating
 PT or killing cancerous, especially non-prostate, cells (e.g. breast
 PT cancerous cells or cancerous cells of metastatic adenocarcinoma to the
 PT liver) -
 XX
 PS Example 12; Column 25; 35pp; English.
 XX
 CC The present invention describes a method of killing cancer cells,
 CC particularly prostate cancer cells, by directing a biological agent to

CC the cells which then binds to a prostate specific membrane antigen and
 CC causes the molecule to be internalised. The internalisation of the agent,
 CC which may be bound to a drug or which may act to kill the cell alone,
 CC then leads to the death of the cell. The present sequence forms
 CC part of an antibody which may be used as the biological agent of the
 CC invention. In addition to prostate cancer, the method can be used with
 CC renal, urothelial, colon, renal, lung and breast cancer cells, and
 CC cancerous cells of metastatic adenocarcinoma to the liver.
 XX Sequence 107 AA;
 SQ

Query Match 100.0%; Score 562; DB 22; Length 107;
 Best Local Similarity 100.0%; Pred. No. 1.2e-39;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NIVMTQSPKSMVSGERVTLTKKASENVVTVSVYQOKPEQSPKLLIYGASNRVTGVPD 60
 Db 1 NIVMTQSPKSMVSGERVTLTKKASENVVTVSVYQOKPEQSPKLLIYGASNRVTGVPD 60
 Qy 61 RFTGSGSATDFTLTISVQAEDLADYHCGQGSYPYTFGGGKLEIK 107
 Db 61 RFTGSGSATDFTLTISVQAEDLADYHCGQGSYPYTFGGGKLEIK 107

RESULT 5
 AAR27144
 ID AAR27144 standard; Protein: 109 AA.
 AC AAR27144;
 XX
 DT 20-MAY-1998 (first entry)
 XX
 DE 1E6 kappa light chain variable region.
 XX
 KW Chimeric; heavy chain; variable region; monoclonal antibody;
 KW lymphocyte function associated antigen-3; LFA-3; inflammation;
 KW autoimmune disease; immunomodulation; systemic lupus erythematosus;
 KW rheumatoid arthritis; thyroiditis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT domain 24..34
 FT /note= "CDR1"
 FT domain 50..56
 FT /note= "CDR2"
 FT domain 89..97
 FT /note= "CDR3"
 XX
 PN EP503646-A.
 XX
 PD 16-SEP-1992.
 XX
 PR 12-MAR-1992; 92EP-0104318.
 XX
 PR 12-MAR-1991; 91US-0667975.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Chisholm PL, Sato VL, Wallner BP;
 DR WPI: 1992-309758/38.
 DR N-PSDB; AAQ28653.
 XX
 PT Monoclonal antibodies active against lymphocyte function
 PT associated antigen-3 - for treating inflammation and auto-immune
 PT diseases, and for detecting LFA-3 protein in a sample
 XX
 PS Claim 19; Page 14; 30pp; English.
 XX
 CC Light and heavy chain variable region sequences were deduced from
 CC the DNA sequences obtd. by PCR of DNA sequences obtd. from the

CC hybridoma cell line 1E6-2C12 (ATCC HB 10693). The light and heavy
 CC chain regions may be used to construct a monoclonal antibody active
 CC against LFA-3 which blocks adhesion of LFA-3 expressing cells to
 CC lymphocytes. The antibody may be used in the treatment and diagnosis
 CC of acute and chronic inflammation, autoimmune diseases and for immuno-
 CC modulation including systemic lupus erythematosus, rheumatoid arthritis
 CC and thyroiditis. See also AAR27145.

XX Sequence 109 AA;

Query Match 100.0%; Score 562; DB 13; Length 109;
 Best Local Similarity 100.0%; Pred. No. 1.3e-39;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMSSVGERVTLTKKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVPD 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 NIVMTQSPKSMSSVGERVTLTKKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVPD 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 61 RFTGSGSATDFTLTISVQAEADLYHCGQGYSPYTFGGGKLEIK 107
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 RFTGSGSATDFTLTISVQAEADLYHCGQGYSPYTFGGGKLEIK 107

RESULT 6

AAW47085
 ID AAW47085 standard; Protein; 121 AA.

XX AAW47085;

DT 26-JUN-1998 (first entry)

XX Mouse J591 monoclonal antibody light chain.

XX Mouse; monoclonal antibody; J591; prostate specific membrane antigen;
 KW cancer; vascular endothelial cell; metastatic adenocarcinoma.

XX Mus sp.

PN W09803873-A1.

XX 29-JAN-1998.

PF 17-JUL-1997; 97WO-US12035.

XX 09-APR-1997; 97US-0838682.

PR 18-JUL-1996; 96US-0022125.

XX (CORR) CORNELL RES FOUND INC.

PA Bander NH;

XX WPI; 1998-120937/11.

DR N-PSDB; AAV13951.

XX Destroying cancer cells with agent that binds to prostate specific
 PT membrane antigen - on vascular endothelial cells near the cancer, or
 PT on normal, hypertrophic or cancerous prostatic cells, also used for
 PT diagnosis

XX Example 12; Page 57; 94pp; English.

XX The present sequence represents the mouse J591 monoclonal antibody light
 CC chain from an example of the present invention. The present invention
 CC describes the elimination of cancer cells by treating vascular
 CC endothelial cells (VEC) close to the cancer with an agent (A) able to
 CC bind to the extracellular domain (ECD) of prostate specific membrane
 CC antigen (PSMA). (A) both binds to the VEC and destroys the cancer cells.
 CC Also described are: (1) the detection of cancer tissue by detecting
 CC binding of labelled (A) to VEC close to, or within, a cancer tissue; (2)
 CC eliminating or detecting normal, benignly hyperplastic or cancerous
 CC prostate epithelial cells using optionally labelled (A); (3) hybridomas
 CC that produce a monoclonal antibody (MAb) that binds to PSMA. The method

CC is used to treat renal, urothelial, colon, lung, rectal or breast
 CC cancers and metastatic adenocarcinoma of the liver. The diagnostic
 CC method is particularly used to detect recurrence of prostatic disease or
 CC to monitor the effect of treatments for prostate cancer (presence of
 CC PSMA in the serum indicates that prostate cells are being lysed). (A)
 CC binds to an epitope of PSMA expressed on live cells (contrast antibody
 CC 7E11 which only binds after cell lysis), allowing targeting of live,
 CC unfixed cells and thus providing more efficient treatment and diagnosis.
 CC Both cancer cells themselves and the VEC on which they depend are
 CC killed. All VEC close to cancer cells express PSMA, whatever the type of
 CC cancer, but normal VEC do not.

XX Sequence 121 AA;

Query Match 100.0%; Score 562; DB 19; Length 121;
 Best Local Similarity 100.0%; Pred. No. 1.4e-39;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMSSVGERVTLTKKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVPD 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 7 NIVMTQSPKSMSSVGERVTLTKKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVPD 66
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 RFTGSGSATDFTLTISVQAEADLYHCGQGYSPYTFGGGKLEIK 107
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 67 RFTGSGSATDFTLTISVQAEADLYHCGQGYSPYTFGGGKLEIK 113

RESULT 7

AAV90370

ID AAV90370 standard; Protein; 121 AA.

XX AAV90370;

DT 15-JAN-2001 (first entry)

XX J591 monoclonal antibody kappa light chain protein sequence #1.

XX J591 monoclonal antibody; extracellular domain; diagnosis; therapy;
 KW prostate specific membrane antigen; prostate cancer; kappa light chain.

XX Homo sapiens.

XX US6107090-A.

XX 22-AUG-2000.

XX 09-APR-1997; 97US-0838682.

XX 06-MAY-1996; 96US-0016976.

PR 18-JUL-1996; 96US-0022125.

XX (CORR) CORNELL RES FOUND INC.

XX Bander NH;

XX WPI; 2000-571325/53.

DR N-PSDB; AAA37832.

XX Antibody specific for extracellular prostate-specific membrane antigen,
 PT useful for diagnosis and treatment of prostate cancer

XX Example 12; Fig 10; 33pp; English.

XX This sequence is the kappa light chain of the monoclonal antibody J591.
 CC The invention relates to an isolated antibody or its antigen binding
 CC portion (I) which binds to an extracellular domain of prostate specific
 CC membrane antigen and which does not require cell lysis to bind to the
 CC extracellular domain. The antibody or its antigen binding portion is
 CC selected for its ability to bind to live cells. (I) is useful for
 CC diagnosis of diseases associated with the presence of normal, benign
 CC hyperplastic, and cancerous epithelial cells or portions. Also it can be
 CC used for identifying the recurrence of such diseases, particularly when

CC the disease is localised in a particular biological material of the
 CC patient for e.g. recurrence of prostatic disease. They can also be used
 CC alone or bound to a substance effective to kill cancerous prostate
 CC epithelial cells as a therapy for prostate cancer. Binding and
 CC internalising of the antibody with the prostate specific membrane
 CC antigen, permits the therapeutic use of intracellularly acting cytotoxic
 CC agents. (1) targets only prostate epithelial cells and other tissue are
 CC spared which provides safer treatment particularly for elderly patients.
 CC The antibodies bind to living prostate cells and treatments using these
 CC antibodies are more effective than those which target lysed prostate
 CC cells.

XX SQ Sequence 121 AA;
 Query Match 100.0%; Score 562; DB 21; Length 121;
 Best Local Similarity 100.0%; Pred. No. 1.4e-39;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NIVMTQSPKSMMSVGERVTLTKASENVTVVSWYQOKPEQSPKLLIYGASNRVTGVPD 60
 Db 7 NIVMTQSPKSMMSVGERVTLTKASENVTVVSWYQOKPEQSPKLLIYGASNRVTGVPD 66
 Qy 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYPTFGGGTKLEIK 107
 Db 67 rftgsgsatdftltissvgaedladyhcgqgysspyptfgggtkleik 113

RESULT 8
 AAB36222
 ID AAB36222 standard; Protein; 121 AA.
 XX AC AAB36222;
 DT 15-FEB-2001 (first entry)
 XX Murine monoclonal antibody J591 kappa light chain #1.
 DE Mouse; antibody; heavy chain; prostate cancer; biological agent.

XX OS Mus sp.
 XX PN US6136311-A.
 XX PD 24-OCT-2000.
 XX PF 17-JUL-1997; 97US-0895914.
 XX PR 06-MAY-1996; 96US-0016976.
 XX PR 18-JUL-1996; 96US-0022125.
 XX PR 09-APR-1997; 97US-0838682.
 XX PA (CORR) CORNELL RES FOUND INC.
 XX PI Bander NH;
 XX DR WPI: 2001-040234/05.
 XX DR N-PSDB; AAC66542.
 PT Use of E99, a J415, a J533 or a J591 monoclonal antibodies for ablating
 PT or killing cancerous, especially non-prostate, cells (e.g. breast
 PT cancerous cells or cancerous cells of metastatic adenocarcinoma to the
 PT liver) -
 XX Example 12; Fig 10; 35pp; English.

XX The present invention describes a method of killing cancer cells,
 CC particularly prostate cancer cells, by directing a biological agent to
 CC the cells which then binds to a prostate specific membrane antigen and
 CC causes the molecule to be internalised. The internalisation of the agent,
 CC which may be bound to a drug or which may act to kill the cell alone,
 CC then leads to the death of the cell. The present sequence forms
 CC part of an antibody which may be used as the biological agent of the

CC invention. In addition to prostate cancer, the method can be used with
 CC renal, uterohelial, colon, renal, lung and breast cancer cells, and
 CC cancerous cells of metastatic adenocarcinoma to the liver.

XX SQ Sequence 121 AA;

Query Match 100.0%; Score 562; DB 22; Length 121;
 Best Local Similarity 100.0%; Pred. No. 1.4e-39;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NIVMTQSPKSMMSVGERVTLTKASENVTVVSWYQOKPEQSPKLLIYGASNRVTGVPD 60
 Db 7 NIVMTQSPKSMMSVGERVTLTKASENVTVVSWYQOKPEQSPKLLIYGASNRVTGVPD 66
 Qy 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYPTFGGGTKLEIK 107
 Db 67 rftgsgsatdftltissvgaedladyhcgqgysspyptfgggtkleik 113

RESULT 9
 AAW01145
 ID AAW01145 standard; Protein; 127 AA.
 XX AC AAW01145;
 DT 10-FEB-1997 (first entry)
 XX MAb 10.1 light chain, directed against type II phospholipase A2.
 DE Monoclonal antibody; phospholipase; myocardial infarction;
 KW pancreatitis; cerebral infarction; acute kidney failure; colitis;
 KW chronic rheumatism; adult respiratory distress syndrome;
 KW cardiac shock; treatment; preclinical testing; disease; hybridoma.
 XX OS Mus musculus.

XX FH Key Location/Qualifiers
 FT Binding-site 44..54
 FT /label= CDR 1
 FT Binding-site 70..76
 FT /label= CDR 2
 FT Binding-site 109..117
 FT /label= CDR 3
 XX WO9620959-A1.
 XX 11-JUL-1996.
 XX 27-DEC-1995; 95WO-JP02714.
 XX 29-DEC-1994; 94JP-0340006.
 XX (YAMA) YAMANOUCHI PHARM CO LTD.
 XX Kawachi Y, Masuho Y, Takasaki J, Yasunaga T;

XX WPI: 1996-333946/33.
 XX DR N-PSDB; AAT40805.
 PT Monoclonal antibody inhibiting type II phospholipase A2 activity -
 PT for treatment of myocardial and cerebral infarction
 XX Claim 6; Figure 13; 69pp; Japanese.

XX Monoclonal antibodies which inhibit type II phospholipase A2 are
 CC useful in the treatment of myocardial infarction, cerebral
 CC infarction, acute kidney failure, chronic rheumatism, cardiac shock,
 CC pancreatitis, adult respiratory distress syndrome and colitis. The
 CC antibodies were generated by immunising Balb/C mice with recombinant
 CC human type II phospholipase A2. Spleen cells from the mice were
 CC fused with mouse myeloma P3U1 (P3x63Ag8.U1) and the hybridomas
 CC obtained were screened for phospholipase A2 inhibitory activity.

CC Active clones were isolated including 12H5, 1.4 and 10.1. These
 CC were cultured and the antibody isolated from the culture
 CC supernatant by precipitation with ammonium sulphate and purification
 CC on a column of protein A-Sepharose CL4B. Because the antibody acts
 CC on the primate and mouse forms of enzyme as well as human it is
 CC particularly suitable for preclinical testing.

XX Sequence 127 AA;

Query Match 100.0%; Score 562; DB 17; Length 127;
 Best Local Similarity 100.0%; Pred. No. 1.5e-39;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMVSIGERVTLTKCKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVPD 60
 DB 21 NIVMTQSPKSMVSIGERVTLTKCKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVPD 80
 QY 61 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYPTFGGKLEIK 107
 DB 81 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYPTFGGKLEIK 127

RESULT 10

AAW01632
 ID AAW01632 standard; Protein; 136 AA.

AC AAW01632;

DT 22-JUL-1997 (first entry)

XX Ber-H2 heavy kappa chain.

DE CD30; immunoglobulin; variable region; CDR; cancer; diagnosis;
 KW therapy; Ber-H2.

XX Homo sapiens.

XX Key Location/Qualifiers

FH Peptide 1..29

FT /label= sig_peptide

FT Protein 30..136

FT /label= mat_protein

XX DE19543039-C1.

XX 21-NOV-1996.

XX 08-NOV-1995; 95DE-1043039.

XX 08-NOV-1995; 95DE-1043039.

XX (MEDA-) MEDAC GES KLINISCHE SPEZIALPRAEPARATE.

XX Stein H, Ziegler A;

XX WPI; 1996-507017/51.

DR N-PSDB; AAT58329.

XX DNA mols. encoding CD30-specific immunoglobulin variable regions -
 PT useful for cancer diagnosis or therapy

XX Claim 15; Page 15; 20pp; German.

XX The ligands are useful for diagnosis or therapy of CD30 expressing
 CC cancers, esp. Hodgkinson's disease.

CC Cytoplasmic RNA was isolated from cells of the mouse myeloma
 CC hybrid line Ber-H2. cDNA was isolated using reverse transcriptase.

CC A VHDJ fragment contg. band was cut from a gel and purified. DNA
 CC corresponding to VK and Vgamma was isolated and cloned into

CC vectors. Oligonucleotides used are given in AAT58331 to AAT58340.

XX Sequence 136 AA;

Query Match 93.8%; Score 527; DB 17; Length 136;
 Best Local Similarity 94.4%; Pred. No. 1.2e-36;
 Matches 101; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMVSIGERVTLTKCKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVPD 60
 DB 30 NIVMTQSPKSMVSIGERVTLTKCKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVPD 89

QY 61 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYPTFGGKLEIK 107
 DB 90 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYPTFGGKLEIK 136

RESULT 11

AA71545
 ID AAY71545 standard; Protein; 127 AA.

XX AAY71545;

DT 12-OCT-2000 (first entry)

XX Mouse AF2 antibody light chain variable region (AF2-VL).

XX Humanised antibody; Hu2AF; mouse AF2 antibody; human EU antibody; AF2-VL;
 KW light chain variable region; VL; heavy chain variable region; VH; IgG2b;
 KW gamma-interferon; IFN; complementarity determining region; CDR; FR;
 KW framework region; immunosuppressive; antiinflammatory; antisclerotic;
 KW gastrointestinal; antidiabetic; antiarthritic; dermatological; inhibitor;
 KW autoimmune disease; graft versus host disease; organ transplant;
 KW multiple sclerosis; Type I diabetes; rheumatoid arthritis; psoriasis;
 KW systemic lupus erythematosus; SLE; Crohn's disease.

XX Mus sp.

XX Key Location/Qualifiers

FH Peptide 1..20

FT /note= "N-terminal peptide"

FT Protein 21..127

FT /note= "Mature mouse antibody AF2 light chain variable
 FT region (AF2-VL)"

FT Region 44..54

FT /label= CDR

FT /note= "Complementarity determining region"

FT Region 70..76

FT /label= CDR

FT /note= "Complementarity determining region"

FT Region 109..117

FT /label= CDR

FT /note= "Complementarity determining region"

XX WO200032634-A1.

XX 08-JUN-2000.

XX 29-NOV-1999; 99WO-US28195.

XX 01-DEC-1998; 98US-0110523.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Vasquez M, Landolfi NF, Tsurushita N, Queen CL;

XX WPI: 2000-412292/35.

DR N-PSDB; AAD01345.

XX Humanized murine AF2 immunoglobulins, useful for inhibiting
 PT gamma-interferon for the treatment of autoimmune diseases, e.g.
 PT multiple sclerosis and diabetes -

XX Claim 1; Fig 1A; 32pp; English.

XX

CC The present amino acid sequence is the mouse AF2 antibody, light chain
 CC variable region (AF2-VL). It has IgG2b isotype and kappa light chain. It
 CC is used for the construction of humanised version of mouse AF2 antibody
 CC HuZAF, that comprises mouse antibody AF2 complementarity determining
 CC regions (CDRs), functionally joined to the human acceptor antibody EU
 CC framework region (FR). HuZAF antibody specifically binds to and
 CC neutralises gamma-interferon (IFN). They can also block the binding of
 CC mouse AF2 immunoglobulin to gamma-IFN. HuZAF does not contain sequences
 CC that are immunogenically active in humans and remains unaffected by
 CC immune responses, that may reduce its activity or circulating half-life.
 CC HuZAF may be administered to treat autoimmune diseases such as graft
 CC versus host disease following organ transplant, Type I diabetes, multiple
 CC sclerosis, rheumatoid arthritis, psoriasis, systemic lupus erythematosus
 CC (SLE), Hashimoto's thyroiditis, primary biliary cirrhosis and
 CC inflammatory bowel disease like, Crohn's disease.

XX SQ Sequence 127 AA;
 Query Match 92.7%; Score 521; DB 21; Length 127;
 Best Local Similarity 91.6%; Pred. No. 3.6e-36;
 Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 NIVMTQSPKSMVSGERVTLTKASENVVTVSVWYQKPEQSPKLLIYGASNRYTGVPD 60
 ||||| :|||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 21 NIVMTQSPKSMVSGERVTLTKASENVVTVSVWYQKPEQSPKLLIYGASNRYTGVPD 80

Qy 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGTGKLEIK 107
 ||||| :|||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 81 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGTGKLEIK 127

RESULT 12
 AAB69693
 ID AAB69693 standard; Protein; 136 AA.

XX AC AAB69693;

XX DT 30-APR-2001 (first entry)

XX DE Murine AF2 antibody light chain SEQ ID NO: 99.

XX KW Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
 KW light chain; graft versus host disease; transplant; autoimmune disease;
 KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
 KW myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.

XX OS Mus sp.

XX PN US6180370-B1.

XX PD 30-JAN-2001.

XX PF 07-JUN-1995; 95US-0484537.

XX PR 28-DEC-1988; 88US-0290975.

XX PR 13-FEB-1989; 89US-0310252.

XX PR 28-SEP-1990; 90US-0590274.

XX PR 19-DEC-1990; 90US-0634278.

XX PA (PROT-) PROTEIN DESIGN LABS INC.

XX PI Queen CL, Selick HE;

XX DR WPI; 2001-190856/19.

XX DR N-PSDB; AAF58757.

XX PT Producing humanized immunoglobulin, involves producing a cell

XX PT containing DNA segments encoding humanized heavy and light chain

XX PT variable regions, and expressing the DNA segments in the cell -

XX PS Example 9; Fig 43; 145pp; English.

XX XX

CC The present invention describes a method of producing humanised
 CC immunoglobulins involving expressing in a cell a nucleic acid encoding a
 CC humanised version of an immunoglobulin. This is obtained by comparing a
 CC donor and human immunoglobulin and producing a combined antibody which
 CC contains part of each. These are useful in the treatment of
 CC graft-versus-host disease, transplant rejection, autoimmune diseases such
 CC as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis
 CC and systemic lupus erythematosus, herpes infections, CMV virus infections
 CC and myeloid leukaemia. The present sequence is an antibody used to
 CC demonstrate the method of the invention.

XX SQ Sequence 136 AA;

Query Match 92.7%; Score 521; DB 22; Length 136;
 Best Local Similarity 91.6%; Pred. No. 3.9e-36;
 Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 NIVMTQSPKSMVSGERVTLTKASENVVTVSVWYQKPEQSPKLLIYGASNRYTGVPD 60
 ||||| :|||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 30 NIVMTQSPKSMVSGERVTLTKASENVVTVSVWYQKPEQSPKLLIYGASNRYTGVPD 89

Qy 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGTGKLEIK 107
 ||||| :|||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 90 RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGGTGKLEIK 136

RESULT 13
 AAW00828

ID AAW00828 standard; Protein; 108 AA.

XX AC AAW00828;

XX DT 19-MAY-1997 (first entry)

XX DE Variable light chain of anti-human Fas ligand antibody NOK-3.

XX KW Variable region; light chain; human; Fas ligand; monoclonal;

XX KW antibody; NOK-3; hybridoma; inhibition; apoptosis; assay;

XX KW diagnosis; disease; hepatitis; infectious mononucleosis;

XX KW systemic lupus erythematosus; ss.

XX OS Mus musculus.

XX PN WO9629350-A1.

XX PD 26-SEP-1996.

XX PF 21-MAR-1996; 96WO-JP00734.

XX PR 27-OCT-1995; 95JP-0303492.

XX PR 20-MAR-1995; 95JP-0087420.

XX PA (SUME) SUMITOMO ELECTRIC IND CO.

XX PI Kayagaki N, Nakata M, Okumura K, Yagita H;

XX XX WPI; 1996-443140/44.

XX DR N-PSDB; AAT39554.

XX XX Monoclonal antibody specifically recognising the Fas ligand - useful

XX PT for the detection of Fas ligands either on cell surface or in

XX PT solution

XX PS Claim 24; Pages 99-100; 133pp; Japanese.

XX CC The present sequence is the light chain variable region of the

XX CC anti-human Fas ligand monoclonal antibody (MAB) NOK-3. NOK-3 is

XX CC produced by the hybridoma NOK-3 (FERM BP-5046), which was prepared

XX CC by immunising mice with transformed human Fas ligand expressing COS

XX CC cells, and fusing spleen cells isolated from the mice with myeloma

XX CC P3x63Ag8.653 (ATCC CRL-1580) cells. The MAB recognises the human

XX CC Fas ligand on the cell surface or in solution, and can be used to

CC Inhibit the apoptosis inducing cell surface Fas ligand/Fas
 CC reaction. The Mab can also be used for a Fas ligand assay in
 CC biological samples (e.g. human blood), especially for disease
 CC diagnosis, e.g. hepatitis, infectious mononucleosis and systemic
 CC lupus erythematosus.
 XX
 SQ Sequence 108 AA;

Query Match 90.6%; Score 509; DB 17; Length 108;
 Best Local Similarity 90.7%; Pred. No. 3e-35;
 Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 NIWMTQSPKMSMSGVGVTVTLCKASENVVTVSWYQQRPEQSPKLLIYGASNRVTGVPD 60

Db 1 NIWMTQSPKMSMSGVGVTVTLCKASENVVTVSWYQQRPEQSPKLLIYGASNRVTGVPD 60

QY 61 RFTGSGSATDFTLTISVQAEADLYHCGGYSPYTFGGGTTKLEIK 107

Db 61 RFTGSGSATDFTLTISVQAEADLYHCGGYSPYTFGGGTTKLEIK 107

RESULT 14

AAR64812
 ID AAR64812 standard; Protein; 239 AA.

XX AC AAR64812;

DT 15-JUL-1995 (first entry)

DE ScFv anti-HCG.

KW ScFv; single chain Fv; HCG; human chorionic gonadotropin;
 KW Aspergillus; Mucor; Neurospora; Penicillium; PUR4138;
 KW monoclonal antibody; Clearblue; fusion protein;
 KW antibody engineering.

OS Mus sp.

FH Key Location/Qualifiers

FT Region 1..119 /label= VH

FT /note= "Mab Clearblue VH region"

FT Region 28..32 /label= CDRI

FT /note= "complementarity determining region 1"

FT Region 47..63 /label= CDRII

FT /note= "complementarity determining region 2"

FT Region 96..108 /label= CDRIII

FT /note= "complementarity determining region 3"

FT Region 120..134 /label= Linker

FT /note= "linker connecting the VH and VL regions"

FT Region 135..239 /label= VL

FT /note= "Mab Clearblue VL region"

FT Region 159..168 /label= CDRI

FT /note= "complementarity determining region 1"

FT Region 184..190 /label= CDRII

FT /note= "complementarity determining region 2"

FT Region 223..230 /label= CDRIII

FT /note= "complementarity determining region 3"

FT Peptide 275..285 /label= Myc_tail

XX W09429457-A.

XX 22-DEC-1994.

XX

XX 09-JUN-1994; 94WO-EP01906.

XX 09-JUN-1993; 93EP-0201660.

PR 09-JUN-1993; 93EP-0201661.

PR 14-JUN-1993; 93EP-0201706.

XX (NEDE) NEDERLAND ORG TNO.

PA (UNIL) UNILEVER NV.

PA (UNIL) UNILEVER PLC.

XX Frerken LGJ, Hessing JGM, Musters W;

PI Vangorcor RFM, Verbakel JMA, Verrips CT, Van Den Hondel CAMJJ;

XX WPI: 1995-036484/05.

DR N-PSDB; AAQ76275.

XX Prodn. of single chain Fv antibody fragments - as fusion proteins

PT using a transformed mould of the genus Aspergillus, Mucor,

PT Neurospora or Penicillium

XX Example 1; Page 13-14; 70pp; English.

XX The PstI-XhoI fragment (given in AAQ76275) of PUR4138 encodes

CC the ScFv fragment (AAR64812) of anti-HCG monoclonal antibody

CC Clearblue.

XX Sequence 239 AA;

Query Match 85.8%; Score 482; DB 16; Length 239;

Best Local Similarity 85.7%; Pred. No. 1.1e-32;

Matches 90; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 NIWMTQSPKMSMSGVGVTVTLCKASENVVTVSWYQQRPEQSPKLLIYGASNRVTGVPD 60

Db 135 dieltgskmsmsvgervtlsckasetvdfsvwygqkpegsplifgsnrfsgvpd 194

QY 61 RFTGSGSATDFTLTISVQAEADLYHCGGYSPYTFGGGTTKLE 105

Db 195 rftgsgsatdftltisvqaedfadyhcgqtnmptyfgggtkle 239

RESULT 15

AAW21939

ID AAW21939 standard; Protein; 107 AA.

XX AC AAW21939;

XX 10-FEB-1998 (first entry)

XX Variable light subunit variant 4 of humanised murine antibody 24-31.

KW Variable light sequence; murine antibody 24-31; gp39; humoral immunity;
 KW activated CD4+ T cell; B cell proliferation; immunodeficiency disease;
 KW human V-kappa subgroup I; DEN; germline 012; rheumatoid arthritis;
 KW multiple sclerosis; diabetes; systemic lupus erythematosus; ITP.

OS Chimeric - Mus sp.

OS Chimeric - Homo sapiens.

XX W09717446-A2.

XX 15-MAY-1997.

XX 07-NOV-1996; 96WO-US17875.

XX 07-NOV-1995; 95US-0554840.

XX (IDEC-) IDEC PHARM CORP.

XX Black A, Hanna N, Newman RA, Padlan EA;

XX

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2001, 09:01:39 ; Search time 25.84 Seconds
(without alignments)
315.429 Million cell updates/sec

Title: US-09-889-300A-2
Perfect score: 562
Sequence: 1 NIVMTQSPKSMMSVGERVT.....CGOGYSPYTFGGGKLEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	562	100.0	136	1 KVM521	Ig kappa chain pre
2	551	98.0	111	2 D37266	Ig kappa chain v r
3	515	91.6	107	2 S33132	Ig kappa chain v r
4	498	88.6	118	2 S3932	Ig kappa chain pre
5	494	87.9	107	2 S38713	Ig light chain v r
6	459	81.7	107	2 PL0268	Ig kappa chain v r
7	454	80.8	96	2 PH1070	Ig light chain v r
8	446.5	79.4	91	2 PH1071	Ig light chain v r
9	440	78.3	108	2 PL0204	anti-DNA autoantib
10	432	76.9	107	2 S32192	Ig kappa chain v r
11	429	76.3	117	2 S42466	Ig kappa chain v r
12	427	76.0	107	2 S32191	Ig kappa chain v r
13	422	75.1	149	1 KVM511	Ig kappa chain pre
14	419	74.6	127	2 S04577	Ig kappa chain pre
15	416	74.0	119	2 P00265	Ig kappa chain v r
16	410	73.0	107	2 A28195	Ig kappa chain v r
17	410	73.0	214	2 S68212	Ig kappa chain (Ma
18	409	72.8	152	2 S30751	Ig kappa chain pre
19	407	72.4	113	2 H30534	Ig kappa chain v r
20	407	72.4	131	2 PL0207	anti-Idiotypic ant
21	404	71.9	113	2 F30534	Ig kappa chain v r
22	403	71.7	114	1 KVM57A	Ig kappa chain v r
23	403	71.7	135	2 S38807	Ig light chain v-J
24	401	71.4	113	2 PL0264	Ig kappa chain v r
25	398.5	70.9	225	2 S37484	Ig kappa chain - m
26	396	70.5	128	2 A47159	Ig lambda chain v
27	395	70.3	107	2 D53285	Ig kappa chain v a
28	395	70.3	112	2 E30538	Ig kappa chain v r
29	395	70.3	112	2 F30538	Ig kappa chain v r

RESULT 1
KVM521
Ig kappa chain precursor V region (MOPC 21) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1980 #sequence_revision 02-Apr-1982 #text_change 22-Jun-1999
C:Accession: A93736; A90262; B49982; A01917
R:Hamlyn, P.H.; Gait, M.J.; Milstein, C.
Nucleic Acids Res. 9, 4485-4494, 1981
A:Title: Complete sequence of an immunoglobulin mRNA using specific priming and the d
A:Reference number: A93736; MUID:82059477
A:Accession: A93736
A:Molecule type: mRNA
R:Residues: 1-136 <HAM>
R:SVast, J.; Milstein, C.
Biochem. J. 128, 427-444, 1972
A:Title: The complete amino acid sequence of a mouse kappa light chain.
A:Reference number: A90262; MUID:73053310
A:Contents: myeloma protein MOPC 21
A:Accession: A90262
A:Molecule type: protein
A:Residues: 30-136 <SVA>
R:Li, C.; Kiebel-Emmons, T.; Villalobos, A.P.; Foster, M.H.; Wahlgren, C.; Kleyman,
J. Biol Chem 269 2805-2813 1994
A:Title: Topology of an anti-idiotype-binding protein.
A:Reference number: A49982; MUID:94132051
A:Accession: B49982
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 30-136 <LIN>
A:Cross-references: GB:L24803; NID:g452098; PIDN:AAC37684.1; PID:g452099
A:Experimental source: clone BA7.1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:superfamily: immunoglobulin v region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-29/Domain: signal sequence #status predicted <STG>
F:30-136/Product: Ig kappa chain V region (MOPC 21) #status experimental <MAT>
F:45-119/Domain: immunoglobulin homology <IMM>
F:125-136/Region: J segment (JK2)
F:52-117/Disulfide bonds: #status predicted

Query Match 100.0%; Score 562; DB 1; Length 136;
Best Local Similarity 100.0%; Pred. No. 2.2e-42;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NIVMTQSPKSMMSVGERVTLTCKASENVVTVSVYQKPEQSPKLLIYGASNRVTGVPD 60
Db 30 NIVMTQSPKSMMSVGERVTLTCKASENVVTVSVYQKPEQSPKLLIYGASNRVTGVPD 89
Qy 61 RFTGSGSATDFTLTSSVOAEDLADYHCGQGYSPYTFGGGKLEIK 107
|||||

ALIGNMENTS

```
Db 90 RFTGSGSATDFTLTISVQAEDLADYHCGGYSYPYTFGGGKLEIK 136
RESULT 2
Ig kappa chain V region (129) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C:Accession: D37266
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A:Title: Heavy and light chain variable region sequences and antibody properties of anti
A:Reference number: A38740; MUID:91177923
A:Accession: D37266
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-111 <RUF>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 98.0%; Score 551; DB 2; Length 111;
Best Local Similarity 98.1%; Pred. No. 1.7e-41;
Matches 105; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIYVTSQPKSMSVSGERVTLTCKASENVVTVSWYQOKPEQSPKLLIYGASNRYTGVPD 60
Db 4 DIVVTQIPKSMSSVSGERVTLTCKASENVVTVSWYQOKPEQSPKLLIYGASNRYTGVPD 63

QY 61 RFTGSGSATDFTLTISVQAEDLADYHCGGYSYPYTFGGGKLEIK 107
Db 64 RFTGSGSATDFTLTISVQAEDLADYHCGGYSYPYTFGGGKLEIK 110

RESULT 3
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S33132
R:Tempest, P.R.; Barbanti, E.; Bremner, P.; Carr, F.J.; Ghislieri, M.; Rifaldi, B.; Marc
submitted to the EMBL Data Library, May 1993
A:Description: A humanized anti-tumor necrosis factor alpha monoclonal antibody that act
A:Reference number: S33131
A:Accession: S33132
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <TEM>
C:Cross-references: EMBL:222670; NID:g297473; PIDN:CAA80379.1; PID:g297474
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 91.6%; Score 515; DB 2; Length 107;
Best Local Similarity 92.5%; Pred. No. 2.2e-38;
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 NIYVTSQPKSMSVSGERVTLTCKASENVVTVSWYQOKPEQSPKLLIYGASNRYTGVPD 60
Db 1 NIYVTSQPKSMSVSGERVTLTCKASENVDTFVSWYQOKPEQSPKLLIYGASNRYTGVPD 60

QY 61 RFTGSGSATDFTLTISVQAEDLADYHCGGYSYPYTFGGGKLEIK 107
Db 61 RFTGSGSATDFTLTISVQAEDLADYHCGGYSYIFPPTLGGGKLEIK 107

RESULT 4
I33932
Ig kappa chain precursor V region (E7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000

C:Accession: I33932
R:Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
A:Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated ger
A:Reference number: A33932; MUID:89282823
A:Accession: I33932
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-118 <BAC>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:39-113/Domain: immunoglobulin homology <IMM>

Query Match 88.6%; Score 498; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 7.5e-37;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIYVTSQPKSMSVSGERVTLTCKASENVVTVSWYQOKPEQSPKLLIYGASNRYTGVPD 60
Db 24 NIYVTSQPKSMSVSGERVTLTCKASENVVTVSWYQOKPEQSPKLLIYGASNRYTGVPD 83

QY 61 RFTGSGSATDFTLTISVQAEDLADYHCGGYSYP 95
Db 84 RFTGSGSATDFTLTISVQAEDLADYHCGGYSYP 118

RESULT 5
Ig light chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C:Accession: S38713
R:Cimani, A.Y.
submitted to the EMBL Data Library, November 1993
A:Reference number: S38713
A:Accession: S38713
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <CIM>
C:Cross-references: EMBL:X76019; NID:g416090; PIDN:CAA53606.1; PID:g1333952
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.9%; Score 494; DB 2; Length 107;
Best Local Similarity 88.8%; Pred. No. 1.5e-36;
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 NIYVTSQPKSMSVSGERVTLTCKASENVVTVSWYQOKPEQSPKLLIYGASNRYTGVPD 60
Db 1 DIVLTSQPKSMSVSGERVTLTCKASENVDTYVSWYQOKPEQSPKLLIYGASNRYTGVE 60

QY 61 RFTGSGSATDFTLTISVQAEDLADYHCGGYSYPYTFGGGKLEIK 107
Db 61 RFTGSGSATDFTLTISVQAEDLADYCGGYSYPLTFGAGTKLEK 107

RESULT 6
PL0268
Ig kappa chain V region (anti-DNA, DP9VK and DP17VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0268
R:Shionochik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A:Reference number: PL0231; MUID:90111618
A:Accession: PL0268
A:Molecule type: mRNA
A:Residues: 1-107 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
```


C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-107/Region: framework 4

Query Match 81.7%; Score 459; DB 2; Length 107;
Best Local Similarity 82.2%; Pred. No. 1.7e-33;
Matches 88; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMVSGERVTLTKKASENVVYVSWYQKPKQSPKLLIYGASNRVTGVPD 60
DB 1 NIVMAWSPKSMVSGERVTLTKKASENVVYVSWYQQTPEQSPKLLIYRASDRYFGVPD 60

QY 61 RFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYPTFGGGTKLEIK 107
DB 61 RFAGSGAADFSLTSSVHAEDLADYCEQSYNPYPTFGGGTKLEVK 107

RESULT 7
PH1070
Ig light chain V region (clone 17s 5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1070
J. Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.
R. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells
A:Reference number: PH0971; MUID:92381444
A:Accession: PH1070
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-96 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.8%; Score 454; DB 2; Length 96;
Best Local Similarity 93.9%; Pred. No. 4.2e-33;
Matches 92; Conservative 1; Mismatches 3; Indels 2; Gaps 2;

QY 1 NIVMTQSPKSMVSGERVTLTKKASENVVYVSWYQKPKQSPKLLIYGASNRVTGVPD 60
DB 1 NIVMTQSPKSMVSGERVTLTKKASENVVYVSWYQKSEQSPKLLIYGASNRVTGVPD 60

QY 61 RFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYPTF 98
DB 61 RFTGSGSATDFTLTSSVQAEADLADYHCGQ-YS-PRTF 96

RESULT 8
PH1071
Ig light chain V region (clone 165.3m) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1071
J. Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.
R. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells
A:Reference number: PH0971; MUID:92381444
A:Accession: PH1071
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-91 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin
F:10-83/Domain: immunoglobulin homology <IMM>

Query Match 79.4%; Score 446.5; DB 2; Length 91;
Best Local Similarity 93.5%; Pred. No. 1.8e-32;
Matches 86; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 7 SPKSMVSGERVTLTKKASENVVYVSWYQKPKQSPKLLIYGASNRVTGVPDRFTGSG 66
DB 1 SPKSMVSGERVTLTKKASENVVYVSWYQKPK-OSPOLLIYGASNRVTGVPDRFTGSG 59

QY 67 SATDFTLTSSVQAEADLADYHCGQGYSPYPTF 98
DB 60 SATDFTLTSSVQAEADLADYHCGQSYSPYPTF 91

RESULT 9
PL0204
anti-DNA autoantibody BV17-45, kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: PL0204
R. Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A:Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from BALB/c mice
A:Reference number: PL0198; MUID:90309768
A:Accession: PL0204
A:Molecule type: mRNA
A:Residues: 1-108 <SMI>
C:Cross-references: GB:X53644; NID:g50198; PIDN:CAA37695.1; PID:g930144
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:50-56/Region: complementarity-determining 2
F:89-97/Region: complementarity-determining 3
F:96-108/Region: JH region

Query Match 78.3%; Score 440; DB 2; Length 108;
Best Local Similarity 79.4%; Pred. No. 7.9e-32;
Matches 85; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMVSGERVTLTKKASENVVYVSWYQKPKQSPKLLIYGASNRVTGVPD 60
DB 1 DIVMTQSPKSMVSGDRVSTCKASQNVVYVSWYQKPKQSPKLLIYGASNRVTGVPD 60

QY 61 RFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYPTFGGGTKLEIK 107
DB 61 RFTGSGSGTDFTLTSSVQSEADLAEYFCQYNSYPYPTFGGGTKLEIK 107

RESULT 10
S32192
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S32192
Rizui, S.
submitted to the EMBL Data Library, February 1993
A:Reference number: S32185
A:Accession: S32192
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <IZU>
A:Cross-references: EMBL:X70097; NID:288262; PIDN:CAA49701.1; PID:g288263
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 432; DB 2; Length 107;
Best Local Similarity 79.4%; Pred. No. 3.9e-31;

```
Matches 85; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 NIYMTQSPKSMMSGVGVTLTKKASENVVTVSWYQKPEQSPKLLIYGASNRVTGVPD 60
:||||| || |||:|||||: |||:||||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DIVMTQSHKFMSTSVGDRVSIITCKASQDVSTAVAWYQKPGQSPKLLIYSASRYTGVPD 60
:||||| ||| |||:|||||: |||:||||| ||| ||| ||| ||| ||| ||| |||
QY 61 RFTGSGSATDFTLTISVQAEDLADYHCQGYSPYPTFGGGTKLEIK 107
||||| ||| |||:|||||: |||:||||| ||| ||| ||| ||| ||| ||| |||
Db 61 RFTGSGSGTDFTTISSVQAEDLAVYVCOQHYSPTPTFGGGTKLEIK 107
||||| ||| |||:|||||: |||:||||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
S42466
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S42466
R:Shiyanov, P.A.; Bespalov, I.A.; Terletskaya, H.N.; Deyev, S.M.
submitted to the EMBL Data Library, March 1994
A:Reference number: S42466
A:Accession: S42466
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-117 <SHI>
A:Cross-references: EMBL:X78108; NID:g460824; PIDN:CAA54998.1; PID:g460825
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 76.3%; Score 429; DB 2; Length 117;
Best Local Similarity 78.5%; Pred. No. 7.8e-31;
Matches 84; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 NIYMTQSPKSMMSGVGVTLTKKASENVVTVSWYQKPEQSPKLLIYGASNRVTGVPD 60
:||||| ||| |||:|||||: |||:||||| ||| ||| ||| ||| ||| ||| |||
Db 11 DIVMTQSHKFMSTSVGDRVSIITCKASQDVSTAVAWYQKPGQSPKLLIYWASRHTGVPD 70
:||||| ||| |||:|||||: |||:||||| ||| ||| ||| ||| ||| ||| |||
QY 61 RFTGSGSATDFTLTISVQAEDLADYHCQGYSPYPTFGGGTKLEIK 107
||||| ||| |||:|||||: |||:||||| ||| ||| ||| ||| ||| ||| |||
Db 71 RFTGSGSGTDFTTISNVQSEDLADYVCOQYSSPYPTFGGGTKLEIK 117
||||| ||| |||:|||||: |||:||||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
S32191
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S32191
R:Izui, S.
submitted to the EMBL Data Library, February 1993
A:Reference number: S32185
A:Accession: S32191
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <ZU>
A:Cross-references: EMBL:X70095; NID:g288260; PIDN:CAA49700.1; PID:g288261
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 427; DB 2; Length 107;
Best Local Similarity 78.5%; Pred. No. 1.1e-30;
Matches 84; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 1 NIYMTQSPKSMMSGVGVTLTKKASENVVTVSWYQKPEQSPKLLIYGASNRVTGVPD 60
:||||| ||| |||:|||||: |||:||||| ||| ||| ||| ||| ||| ||| |||
Db 1 DIVMTQSHKFMSTSVGDRVSIITCKASQDVSTAVAWYQKPGQSPKLLIYSASRYTGVPD 60
:||||| ||| |||:|||||: |||:||||| ||| ||| ||| ||| ||| ||| |||
QY 61 RFTGSGSATDFTLTISVQAEDLADYHCQGYSPYPTFGGGTKLEIK 107
||||| ||| |||:|||||: |||:||||| ||| ||| ||| ||| ||| ||| |||
Db 61 RFTGSGSGTDFTTISSVQPEDLAVYVCOQHYSPTPTFGGGTKLEIK 107
||||| ||| |||:|||||: |||:||||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 13
KVMS11
Ig kappa chain precursor V region (MPC11) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 21-Jan-2000
C:Accession: A90823; A90753; A90298; A01916
R:Kelley, D.E.; Coleclough, C.; Perry, R.P.
Cell 29, 681-689, 1982
A:Title: Functional significance and evolutionary development of the 5'-terminal regi
A:Reference number: A90823; MUID:83001944
A:Accession: A90823
A:Molecule type: DNA
A:Residues: 1-71 <REL>
A>Note: The sequence was determined from the differentiated gene
R:Rabbits, T.H.; Hamlyn, P.H.; Matthysens, G.; Roe, B.A.
Can. J. Biochem. 58, 176-187, 1980
A:Title: The variability, arrangement, and rearrangement of immunoglobulin genes.
A:Reference number: A90753; MUID:80176554
A:Accession: A90753
A:Molecule type: mRNA
A:Residues: 41-149 <RAB>
R:Smith, G.P.
Biochem. J. 171, 337-347, 1978
A:Title: Sequence of the full-length immunoglobulin kappa-chain of mouse myeloma MPC
A:Reference number: A90298; MUID:78186617
A:Contents: myeloma protein MPC11
A:Accession: A90298
A:Molecule type: protein
A:Residues: 30-149 <SMI>
A>Note: the amidation states of residues 58, 69, 101, 111, 120, 122, and 123 were not
C:Comment: The mature chain has 12 additional residues at its amino end, due to a tan
42 corresponds to the amino-terminal residue of typical kappa chains.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: duplication; heterotetramer; immunoglobulin
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-149/Product: Ig kappa chain V region (MPC11) #status experimental <MAT>
F:57-131/Domain: immunoglobulin homology <IMM>
F:64-129/Disulfide bonds: #status predicted
```

```
Query Match 75.1%; Score 422; DB 1; Length 149;
Best Local Similarity 78.5%; Pred. No. 4e-30;
Matches 84; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 1 NIYMTQSPKSMMSGVGVTLTKKASENVVTVSWYQKPEQSPKLLIYGASNRVTGVPD 60
:||||| ||| |||:|||||: |||:||||| ||| ||| ||| ||| ||| ||| |||
Db 42 DIVMTQSHKFMSTSVGDRVSIITCKASQDVSTAVAWYQKPGQSPKLLIYSASRYTGVPD 101
:||||| ||| |||:|||||: |||:||||| ||| ||| ||| ||| ||| ||| |||
QY 61 RFTGSGSATDFTLTISVQAEDLADYHCQGYSPYPTFGGGTKLEIK 107
||||| ||| |||:|||||: |||:||||| ||| ||| ||| ||| ||| ||| |||
Db 102 RFTGSGSGTDFTTISSVQAEDLAVYVCOQHYSPTPTFGGGTKLEIK 148
||||| ||| |||:|||||: |||:||||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
S04577
Ig kappa chain precursor V region (MRL-RF28L) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: S04577
R:Kofler, R.; Duchosal, M.A.; Dixon, F.J.
submitted to the EMBL Data Library, March 1989
A:Description: Complexity, polymorphism and connectivity of murine V(kappa) gene fami
A:Reference number: S04577
A:Accession: S04577
A:Molecule type: mRNA
A:Residues: 1-127 <KOF>
A:Cross-references: EMBL:X14622; NID:g52400; PIDN:CAA32775.1; PID:g52401
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
```


THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2001, 09:03:06 ; Search time 22.67 seconds
(without alignments)
106.213 Million cell updates/sec

Title: US-09-889-300A-2

Perfect score: 562

Sequence: 1 NIVMTQSPKMSMSVGRVT.....CGQGYSPYPTFGGTKLEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Capext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	562	100.0	107	3	US-08-838-682-16
2	562	100.0	107	4	US-08-895-914-16
3	562	100.0	107	4	US-09-357-710A-16
4	562	100.0	109	5	PCT-US92-02044-2
5	562	100.0	121	3	US-08-838-682-11
6	562	100.0	121	4	US-08-895-914-11
7	562	100.0	121	4	US-09-357-710A-11
8	521	92.7	136	1	US-07-634-278-99
9	521	92.7	136	1	US-08-477-728-99
10	521	92.7	136	1	US-08-474-040-99
11	521	92.7	136	1	US-08-487-200-99
12	521	92.7	136	4	US-08-484-537-99
13	454	80.8	107	3	US-08-554-840-4
14	449	79.9	107	3	US-08-554-840-2
15	447	79.5	107	3	US-08-554-840-3
16	444	79.0	107	3	US-08-554-840-1
17	441	78.5	107	1	US-07-634-278-103
18	441	78.5	107	1	US-08-477-728-103
19	441	78.5	107	1	US-08-474-040-103
20	441	78.5	107	1	US-08-487-200-103
21	441	78.5	107	4	US-08-484-537-103
22	426	75.8	108	4	US-09-157-370-4
23	424.5	75.5	108	2	US-08-657-012-25
24	424.5	75.5	108	3	US-09-013-872-25
25	424.5	75.5	108	4	US-09-184-198-25
26	424	75.4	249	2	US-08-797-689-18
27	423	75.3	108	4	US-08-752-693A-1

28 423 75.3 132 1 US-08-253-877C-55 Sequence 55, Appl
29 423 75.3 132 2 US-08-452-164A-55 Sequence 55, Appl
30 423 75.3 132 4 US-08-976-183A-36 Sequence 36, Appl
31 423 75.3 132 4 US-08-976-183A-37 Sequence 37, Appl
32 422 75.1 237 2 US-08-224-591-16 Sequence 16, Appl
33 422 75.1 237 2 US-08-926-789-16 Sequence 16, Appl
34 422 75.1 241 2 US-08-224-591-18 Sequence 18, Appl
35 422 75.1 241 2 US-08-926-789-18 Sequence 18, Appl
36 420 74.7 147 2 US-08-653-402B-4 Sequence 4, Appl
37 419 74.6 250 1 US-08-133-804-2 Sequence 2, Appl
38 419 74.6 250 1 US-08-461-184-8 Sequence 8, Appl
39 419 74.6 250 1 US-08-463-675-8 Sequence 8, Appl
40 419 74.6 250 1 US-08-464-589-8 Sequence 8, Appl
41 419 74.6 250 1 US-08-461-838-2 Sequence 2, Appl
42 419 74.6 250 2 US-08-461-386-2 Sequence 2, Appl
43 418.5 74.5 124 3 US-08-466-151-4 Sequence 4, Appl
44 416 74.0 106 2 US-08-822-830B-4 Sequence 4, Appl
45 416 74.0 106 2 US-08-950-660-4 Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-838-682-16
; Sequence 16, Application US/08838682
; Patent No. 6107090
; GENERAL INFORMATION:
; APPLICANT: Gander M.D., Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE
; TITLE OF INVENTION: CANCER
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603-1051
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,682
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/016,976
; FILING DATE: 06-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/022,125
; FILING DATE: 18-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1172
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-682-16

Query Match 100.0%; Score 562; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-50;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIVMTSPKSMSSVGERVTLTKASENVVTVSWYQKPEQSPKLLIYGASNRVTGVPD 60
 DB 1 NIVMTSPKSMSSVGERVTLTKASENVVTVSWYQKPEQSPKLLIYGASNRVTGVPD 60
 QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGGYSYPTFTGGTGLEIK 107
 DB 61 RFTGSGSATDFTLTISVQAEADLADYHCGGYSYPTFTGGTGLEIK 107

RESULT 2

US-08-895-914-16
 ; Sequence 16, Application US/08895914
 ; Patent No. 6136311
 ; GENERAL INFORMATION:
 ; APPLICANT: Bander, Neil H.
 ; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
 ; STREET: Clinton Square, P.O. Box 1051
 ; CITY: Rochester
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 14603-1051
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/895,914
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/016,976
 ; FILING DATE: 06-MAY-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/022,125
 ; FILING DATE: 18-JUL-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/838,682
 ; FILING DATE: 09-APR-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Goldman, Michael L.
 ; REGISTRATION NUMBER: 30,727
 ; REFERENCE/DOCKET NUMBER: 19603/1173
 ; TELEPHONE: (716) 263-1304
 ; TELEFAX: (716) 263-1600
 ; INFORMATION FOR SEQ ID NO: 16:
 ; LENGTH: 107 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-895-914-16

Query Match 100.0%; Score 562; DB 4; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.7e-50;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NIVMTSPKSMSSVGERVTLTKASENVVTVSWYQKPEQSPKLLIYGASNRVTGVPD 60
 DB 1 NIVMTSPKSMSSVGERVTLTKASENVVTVSWYQKPEQSPKLLIYGASNRVTGVPD 60
 QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGGYSYPTFTGGTGLEIK 107
 DB 61 RFTGSGSATDFTLTISVQAEADLADYHCGGYSYPTFTGGTGLEIK 107

RESULT 3

US-09-357-710A-16
 ; Sequence 16, Application US/09357710A
 ; Patent No. 6290956
 ; GENERAL INFORMATION:
 ; APPLICANT: Bander, Neil H.
 ; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: Lois M. Kwasigroch; BZL 242/025
 ; CURRENT APPLICATION NUMBER: US/09/357,710A
 ; CURRENT FILING DATE: 1999-07-20
 ; PRIOR APPLICATION NUMBER: US 08/838,682
 ; PRIOR FILING DATE: 1997-04-09
 ; PRIOR APPLICATION NUMBER: US 60/016,976
 ; PRIOR FILING DATE: 1996-05-06
 ; PRIOR APPLICATION NUMBER: US 60/022,125
 ; PRIOR FILING DATE: 1996-07-18
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: Patent In version 3.0
 ; SEQ ID NO: 16
 ; LENGTH: 107
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 ; US-09-357-710A-16

Query Match 100.0%; Score 562; DB 4; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.7e-50;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NIVMTSPKSMSSVGERVTLTKASENVVTVSWYQKPEQSPKLLIYGASNRVTGVPD 60
 DB 1 NIVMTSPKSMSSVGERVTLTKASENVVTVSWYQKPEQSPKLLIYGASNRVTGVPD 60
 QY 61 RFTGSGSATDFTLTISVQAEADLADYHCGGYSYPTFTGGTGLEIK 107
 DB 61 RFTGSGSATDFTLTISVQAEADLADYHCGGYSYPTFTGGTGLEIK 107

RESULT 4

PCT-US92-02044-2
 ; Sequence 2, Application PC/TUS9202044
 ; GENERAL INFORMATION:
 ; APPLICANT: BHOGEN, INC.
 ; APPLICANT: SATO, Vicki L.
 ; APPLICANT: CHISHOLM, Patricia L.
 ; APPLICANT: WALLNER, Barbara P.
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODIES RECOGNIZING
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: c/o FISH & NEAVE
 ; STREET: 875 Third Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US92/02044
 ; FILING DATE: 19920312-2
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/667,975
 ; FILING DATE: 12-MAR-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: HALEY Jr., James F.
 ; REGISTRATION NUMBER: 27,794
 ; REFERENCE/DOCKET NUMBER: B150CIP

```

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 60/016,976
  FILING DATE: 06-MAY-1996
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 60/022,125
  FILING DATE: 18-JUL-1996
  ATTORNEY/AGENT INFORMATION:
    NAME: Goldman, Michael L.
    REGISTRATION NUMBER: 30,727
    REFERENCE/DOCKET NUMBER: 19603/1172
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (716) 263-1304
  TELEFAX: (716) 263-1600
  INFORMATION FOR SEQ ID NO: 11:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 121 amino acids
      TYPE: amino acid
      STRANDEDNESS:
        TOPOLOGY: linear
      MOLECULE TYPE: protein
  US-08-838-682-11

```

Qy	1	NIWMTQSPKSMVSIGERVITLTCASENVTYYSWYQOQPEQSPKLLIYGASNRYTGVPD	60
Db	7	NIWMTQSPKSMVSIGERVITLTCASENVTYYSWYQOQPEQSPKLLIYGASNRYTGVPD	66
Qy	61	RTFGSGATDFTLTISVQOAEADLYHCGGCGYSYPTTFGGTKEIK	107

Db 67 RFTGSGSATDTLTISVQAEDLADYHCGGYSYPYTFGGGTKEIK 113
|||||
RESULT 7
US-09-357-710A-11
; Sequence 11, Application US/09357710A
; Patent No. 6290956
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: Lois M. Kwasiroch: BZL 242/025
; CURRENT APPLICATION NUMBER: US/09/357,710A
; CURRENT FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-357-710A-11

Query Match 100.0%; Score 562; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.9e-50;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NIYVOTSPKSMVSGERVTLTCKASENVVTVYVSWYQOQPEQSPKLLIYGASNRITGVDP 60
Db 7 NIYVOTSPKSMVSGERVTLTCKASENVVTVYVSWYQOQPEQSPKLLIYGASNRITGVDP 66
QY 61 RFTGSGSATDTLTISVQAEDLADYHCGGYSYPYTFGGGTKEIK 107
Db 67 RFTGSGSATDTLTISVQAEDLADYHCGGYSYPYTFGGGTKEIK 113

RESULT 8
US-07-634-278-99
; Sequence 99, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274

; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-634-278-99
Query Match 92.7%; Score 521; DB 1; Length 136;
Best Local Similarity 91.6%; Pred. No. 3.3e-46;
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 NIYVOTSPKSMVSGERVTLTCKASENVVTVYVSWYQOQPEQSPKLLIYGASNRITGVDP 60
Db 30 NIYVOTSPKSMVSGERVTLTCKASENVDTYVSWYQOQPEQSPKLLIYGASNRITGVDP 89
QY 61 RFTGSGSATDTLTISVQAEDLADYHCGGYSYPYTFGGGTKEIK 107
Db 90 RFTGSGSATDTLTISVQAEDLADYHCGGYSYNYPYTFGGGTKEIK 136
RESULT 9
US-08-477-728-99
; Sequence 99, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975


```

Query Match      80.88; Score 454; DB 3; Length 107;
Best Local Similarity 80.48; Pred. No. 1.7e-39;
Matches 86; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 NVNVTQSPKSMSSVGERVLTCTKASENVVTYVSWYQOKPEQSPKLLIYGASNRYTGVPD 60
      ||||| ||| : ||||| ||| : ||||| ||| : ||||| ||| : ||||| ||| :
Db 1 DIVMTQSPDMSATSLGERVTTNCKASONTAVTAVMYQOKGQSPKLLIYASNRYTGVPD 60
      ||||| ||| : ||||| ||| : ||||| ||| : ||||| ||| : ||||| ||| :

QY 61 RFTGSGSATDFTLLISSVQARDLADYHCGGGYSYPYTFGGTGKLEIK 107

```
